

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 13, 2005, 01:11:37 ; Search time 6621 Seconds
(without alignments)
11321.586 Million cell updates/sec

Title: US-09-869-079b-1

Perfect score: 1547

Sequence: 1 gggagtcacatcagcagcagatg.....tcttacacatcagcaggggcca 1547

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hng:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	1547	6	BD251226 Human Akt
2	1547	100.0	1547	6	AX026529 Sequence
3	1547	100.0	1547	9	HS245709 Homo sapi
4	1547	100.0	1706	9	AF085234 Homo sapi
5	1545.4	99.9	1708	9	AF124141 Homo sapi
6	1544.4	99.8	2367	6	BD260777 Homo sapi
7	1537	99.4	2811	9	AF135794 Homo sapi
8	1492	96.4	1651	6	CQ714620 Sequence
9	1490	93.1	1440	6	BD142211 Method to
10	1438	93.0	1440	12	AY335691 Synthetic
11	1434.4	92.7	1436	6	BD251227 Human Akt
12	1434.4	92.7	1436	6	AX026530 Sequence
13	1364.8	88.2	1570	6	BD250154 AKT nucle
14	1364.8	88.2	1570	6	AX056819 Sequence
15	1364.8	88.2	1570	6	AX251592 Sequence
16	1364.8	88.2	1584	9	AL117525 Homo sapi
17	1364.8	87.8	1695	9	AY005799 Homo sapi
18	1358.8	87.8	1760	10	AF124142 Mus muscu
19	1355.6	87.6	4751	10	BC066861 Mus muscu

20	1234.8	79.8	1548	10	RATRAPKC	D49836 Rat mRNA fo
21	850.6	55.0	2277	5	AF039943	AF039943 Gallus ga
22	789.2	51.0	1808	5	AF317656	AF317656 Xenopus l
23	769.2	49.7	1052	5	BX950472	BX950472 Gallus ga
24	754.6	48.8	3536	14	AKTAKTA	M80675 AKT8 provir
25	751.4	48.6	2626	6	BD270825	BD270825 AKT compo
26	751.4	48.6	2626	6	AR474029	AR474029 Sequence
27	751.4	48.6	2626	10	MMSTPK	X65687 M.musculus
28	746.6	48.3	1513	10	MUSRAC	M94335 Mus musculu
29	746.6	48.3	2701	10	BC066018	BC066018 Mus muscu
30	738.2	47.7	4181	5	BC072041	BC072041 Xenopus l
31	729	47.1	1617	5	RATRPXA	D30040 Rat mRNA fo
32	723.4	46.8	3347	5	BC046261	BC046261 Xenopus l
33	722.4	46.7	2729	9	BC000479	BC000479 Homo sapi
34	722.4	46.7	3410	6	HS245709	BX648205 Homo sapi
35	721.2	46.6	2184	6	A84523	A84523 Sequence 13
36	721.2	46.6	2184	6	CO830047	CO830047 Sequence
37	721.2	46.6	2184	6	AR279966	AR279966 Sequence
38	721.2	46.6	2184	6	AX427442	AX427442 Sequence
39	721.2	46.6	2184	6	BD082588	BD082588 A method
40	720.8	46.6	2868	9	BC084538	BC084538 Homo sapi
41	720.8	46.6	3913	9	AK122894	AK122894 Homo sapi
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43	719.2	46.5	2610	6	A62733	A62733 Sequence 3
44	719.2	46.5	2610	6	A63232	A63232 Sequence 1
45	719.2	46.5	2610	6	AR076381	AR076381 Sequence

ALIGNMENTS

RESULT 1	BD251226	Human Akt-3.	1547 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD251226	Human Akt-3.				
DEFINITION	BD251226	Human Akt-3.				
ACCESSION	BD251226.1	GI:33060996				
VERSION	BD251226.1	GI:33060996				
KEYWORDS	JP 2002535964-A/1.					
SOURCE	JP 2002535964-A/1.					
ORGANISM	Homo sapiens (human)					
REFERENCE	1 (bases 1 to 1547)					
AUTHORS	Masure,S.L.J. and Richardson,A.					
TITLE	Human Akt-3					
JOURNAL	Patent: JP 2002535964-A 1 29-OCT-2002;					
COMMENT	JANSEN PHARMACEUTICAL NV					
OS	Homo sapiens (human)					
PN	JP 2002535964-A/1					
PD	29-OCT-2002					
PF	17-DEC-1999 JP 2000589669					
PR	22-DEC-1998 GB 9828375.7					
PI	STEFAN LEO JOZEF MASURE,ALAN RICHARDSON					
PC	C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K48/00, PC					
	A61P35/00,					
PC	A61P43/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/					
PC	12,C12O1/02,					
PC	C12Q1/48,G01N33/15,G01N33/50,G01N33/53,G01N33/566//C12P21/08,					
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PC	C12N5/00,A61K37/60					
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CC	Human Akt-3					
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Query Match	100.0%; Score 1547; DB 6; Length 1547;					

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0;
Indels 0; Gaps 0

Oy	1	GGAGTCACTCATGACGAGTGTATACCATTTGTGAAGAAGTTGGTTCGAAACAGGGGAGA	60
Db	1	GGAGTCACTCATGACGAGTGTATACCATTTGTGAAGAAGTTGGTTCGAAACAGGGGAGA	60
Oy	61	ATATATAAAACTGAGGCCAAGATACTCTCTTTTGAAGACAGATGGCTCATTCATAG	120
Db	61	ATATATAAAACTGAGGCCAAGATACTCTCTTTTGAAGACAGATGGCTCATTCATAG	120
Oy	121	ATATTAAGAAGAACTCTCAAGATGTGTGATTTTACCTTATGCCCTCAACAACCTTTTCATGTGC	180
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Oy	181	AAAAATGCAGTTAATGAAGAAACGAAGCAGACCAAGGCCAAACACATTTATPAATCAGATGTC	240
Db	181	AAAAATGCAGTTAATGAAGAAACGAAGCAGACCAAGGCCAAACACATTTATPAATGATGTC	240
Oy	241	CCAGTGAACCTACTGTTATAGAGAGAACTTTCATGTAGATACTCCAGAGGAAAGGAGAGA	300
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Oy	301	ATGACAGAGACTATCCAGGCTGTGACAGACGACTGACAGGCGCAAGAGAGAGAGAT	360
Db	301	ATGACAGAGACTATCCAGGCTGTGACAGACGACTGACAGGCGCAAGAGAGAGAGAT	360
Oy	361	GAATGTGTGCCAATTCGACAAATTGATATATATAGAGAGGAAAGATGAGATGCTCTAC	420
Db	361	GAATGTGTGCCAATTCGACAAATTGATATATATAGAGAGGAAAGATGAGATGCTCTAC	420
Oy	421	AACCCATCATAAAGAGAAACATAGATGATTTTGAATCTATTTGAAACTATAGATTAAG	480
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Oy	541	GATTCGAGAAAGAGTCATTATTTGCAAGAGATGAAAGTGGCAGACACTTACTGATGAA	600
Db	541	GATTCGAGAAAGAGTCATTATTTGCAAGAGATGAAAGTGGCAGACACTTACTGATGAA	600
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Db	721	GTGAGAGAGGGGGTCTCTGAGAGACCGACACGTTTCTATGATGAGAAATGTGTC	780
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Db	781	TGCCTTGACTATCTACATTCGGAAGAAATGTGTACCGTGATCTCAAGTTGGAATCT	840
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Db	841	AATGCTGACAAAGATGGCCACATTAATAATTCAGATTTTGGACCTTTCAGAAAGGAGAT	900
Oy	901	CACAGATCAGACCAATGAAGACATTCGTGGGCACTCCAGAAATCTGGGCAACGAGAT	960
Db	901	CACAGATCAGACCAATGAAGACATTCGTGGGCACTCCAGAAATCTGGGCAACGAGAT	960
Oy	961	GTTAGAAATATGACTATGGCCGAGCAGTATGACTGTGGGGCTTAGGGGTTGTATGTA	1020
Db	961	GTTAGAAATATGACTATGGCCGAGCAGTATGACTGTGGGGCTTAGGGGTTGTATGTA	1020
Oy	1021	TGAAATGATGTGTGGAGTTACTTTTCAACACGAGACCATGAGAACTTTTGAATT	1080

Db	1021	GGAAATGATGTGTGGAGGTTACCTTTCTTCAACACGAGACCATGAGAAACCTTTTGAATT	1080
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Db	1081	AATATTATGAGAGACATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCT	1140
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Db	1141	TTGAGGGCTCTGTGTAAGAATCCAAATPAAACGGCTTGGTGGAGACAGATGATGCAAA	1200
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Qy	1321	AGATTTTACAGCTTCAGACTATTTACAAATPAAACCACTGAAAAAATATGATGAGATGGTAT	1380
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Db	1381	GGAATGATGAGACAAATAGAGGGGGCGGCAATTTCCCTCAATTTTCTACTCTGCAAGTGG	1440
Qy	1441	ACGAGAAATGAAGTCTCTTTCAATTTCTGTACTTCACTGATCATTTGCAATTTATCTGAAAA	1500
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Qy	1501	TGATTCCTGACATCACCACTGCTCTTACACATAGCAGGGGCA	1547
Db	1501	TGATTCCTGACATCACCACTGCTCTTACACATAGCAGGGGCA	1547
RESULT 2			
AX026529			
LOCUS	AX026529	1547 bp	DNA
DEFINITION	Sequence 1 from Patent WO0037613.	linear	PAT 16-SEP-2000
ACCESSION	AX026529		
VERSION	AX026529.1	GI:10187717	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Ekukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	Mesure, S.L. and Richardson, A.		
	Human akt-3		
	Patent: WO 0037613-A 1 29-JUN-2000;		
	MAJURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN		
	PHARMACEUTICA NV (BE)		
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	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 1547; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	1	GGGAGTATGATGAGCGATGTACCATTTGTAAGAAAGAGTTGGTTGAGAAAGAGGGGAGA	60
Db	1	GGGAGTATGATGAGCGATGTACCATTTGTAAGAAAGAGTTGGTTGAGAAAGAGGGGAGA	60
Qy	61	ATATATATAAAAACTGAGGCGCAAGATATCTCTTTTGAAGACAGATGGCTCATATAGG	120
Db	61	ATATATATAAAAACTGAGGCGCAAGATATCTCTTTTGAAGACAGATGGCTCATATAGG	120
Qy	121	ATATTAAGAGAAACCTCAAGATGTGATTTACCTTATCCCTCAACAACCTTTTCAGTGC	180

Db 121 ATATAAAGAAACCTCAGATGTGATTACCTTATCCCTCAACAACATTTTCAGTGGC 180
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 QY 1321 AGAATTTACAGCTCAGACTATTACATAACACCACTGAAATAATGATGAGATGATAT 1380
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 Db 1441 AGGAGAAATAGTCTCTTTCATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1500
 QY 1501 TGATTCCTGACATCACAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTG 1547
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RESULT 3
 HSA245709
 LOCUS
 DEFINITION Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).
 ACCESSION AJ245709.1 GI:5804885
 VERSION AJ245709.1 GI:5804885
 KEYWORDS Akt-3; Akt3 gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 2 (bases 1 to 1547)
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Phosphorylation at Thr305 and at Ser472 necessary for activation.
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3' UTR

ORIGIN

Query Match	100.0%	Score 1547	DB 9	Length 1547
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DB	61	ATATATATAAACTGGAGGCCAAGATACCTCTTTTGAAGACAGATGGCTCATTTAGG	120	
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DB	121	ATATATAAGAAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGC	180	
QY	181	AAAATGCCAGTTAATGAAAACAGAACCAAGCCAAACACATTTATATGAGATGCT	240	
DB	181	AAAATGCCAGTTAATGAAAACAGAACCAAGCCAAACACATTTATATGAGATGCT	240	
QY	241	CGAGTGGACTACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGAAAGGAGA	300	
DB	241	CGAGTGGACTACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGAAAGGAGA	300	
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QY	481	CACTTTGGGAAAGTATTTGGTTGGAGAGAAAGCAAGTGAATACTATGCTATGAA	540	
DB	481	CACTTTGGGAAAGTATTTGGTTGGAGAGAAAGCAAGTGAATACTATGCTATGAA	540	
QY	541	GATTCGAGAAAGAGATCATTTATGCAAAAGATGAGTGACACACTCTAACTGAAG	600	
DB	541	GATTCGAGAAAGAGATCATTTATGCAAAAGATGAGTGACACACTCTAACTGAAG	600	
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QY	661	AAAAGACGTTGTGTTGTGATGAGATATGTTATGGGGGAGAGCTGTTTCCATTT	720	
DB	661	AAAAGACGTTGTGTTGTGATGAGATATGTTATGGGGGAGAGCTGTTTCCATTT	720	
QY	721	GTCGAGAGAGCGGGTCTCTGAGAGACGACACCTTTCTATGTCGAGAAATTTCTC	780	
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QY	781	TGCTTGGACTATCTATCCGGAAGATTTGTATCCGTGATCTCAAGTTGGAATCT	840	
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QY	841	AATGCTGGAAGAGATGGCCATATAAATATACAGATTTTGACCTTTGCAAAAGAGAT	900	
DB	841	AATGCTGGAAGAGATGGCCATATAAATATACAGATTTTGACCTTTGCAAAAGAGAT	900	

QY	901	CACAGATGAGCGACACCATGAGACATCTGTGGACCTCCAGAAATATCTGGACAGAGT	960	
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DEFINITION AF085234				
ACCESSION AF085234				
VERSION AF085234.1 GI:17529662				
KEYWORDS				
SOURCE				
ORGANISM Homo sapiens (human)				
REFERENCE				
AUTHORS Li, X., Yu, L., Huang, H., Zhang, M., Zhao, Y., and Zhao, S.				
TITLE Cloning of a novel human cDNA, STK-2, which encodes a rat				
JOURNAL Unpublished				
REFERENCE				
AUTHORS Zhao, Y.				
JOURNAL Direct Submission				
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ORIGIN

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RESULT 5
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 ACCESSION AF124141
 VERSION AF124141.1 GI:4757578
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1708)
 Brodebeck,D., Cron,P. and Hemmings,B.A.
 A human protein kinase Bgamma with regulatory phosphorylation sites
 in the activation loop and in the C-terminal hydrophobic domain
 J. Biol. Chem. 274 (14), 9133-9136 (1999)
 JOURNAL 59194749
 MEDLINE 10092583
 PUBMED 2 (bases 1 to 1708)
 REFERENCE Brodebeck,D., Cron,P. and Hemmings,B.A.
 AUTHORS Direct Submission
 TITLE

JOURNAL Submitted (27-JAN-1999) Friedrich Miescher-Institut,

Maubecstrasse 66, Basel 4058, Switzerland

FEATURES

source

CDS

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Query Match 99.9%; Score 1545.4; DB 9; Length 1708;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6

BD260777

LOCUS

DEFINITION

human protein kinase B-gamma

nonhuman protein kinase B-gamma.

ACCESSION

BD260777

VERSION

BD260777.1 GI:33070547

KEYWORDS

JP 2002539823-A/1.

SOURCE

ORGANISM

REFERENCE

Human protein kinase B-gamma polypeptide and method of degrading

nonhuman protein kinase B-gamma.

human protein kinase B-gamma.

human protein kinase B-gamma.

human protein kinase B-gamma.

human protein kinase B-gamma.

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human protein kinase B-gamma.

human protein kinase B-gamma.

AUTHORS
TITLE
JOURNAL
COMMENT
Biovitrum AB
OS Homo sapiens (human)
PN JP 2002539823-A/1
PD 26-NOV-2002
PR 23-MAR-2000 JP 2000608727
PR 25-MAR-1999 SE 9901115-7
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RESULT 7
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DEFINITION Homo sapiens AKT3 protein kinase mRNA, complete cds.
ACCESSION AP135794
VERSION AP135794.1 GI:4574743
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 2811)
AUTHORS Nakatani, K., Sakaue, H., Thompson, D.A., Weigel, R.J. and Roth, R.A.
TITLE Identification of a human Akt3 (protein kinase B gamma) which
contains the regulatory serine phosphorylation site
JOURNAL Biochem. Biophys. Res. Commun. 257 (3), 906-910 (1999)
MEDLINE 9925329
PUBMED 10208883
REFERENCE 2 (bases 1 to 2811)
AUTHORS Thompson, D.A., Nakatani, K. and Sakaue, H.
TITLE Direct Submission
JOURNAL Published (18-MAR-1999) Surgery, MSIS Building, Room P228, 1201
Welch Road, Stanford, CA 94305, USA
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RESULT 8
LOCUS COJ14620
DEFINITION Sequence 554 from Patent WO02068579.
ACCESSION COJ14620
VERSION COJ14620
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
Kites, such as nucleic acid arrays, comprising a majority of
humaneons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 554 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1016 ATGTATGAATGATGTGTGGAGGTTACCTTTCTACACAGAGACCATGAGAACTTTT 1075
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BD142211 1440 bp DNA linear PAT 18-SEP-2002
LOCUS BD142211
DEFINITION Method for controlling apoptosis and polypeptide controlling
apoptosis.
ACCESSION BD142211
VERSION BD142211.1 GI:23237156
KEYWORDS WO 0215925-A/5
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1440)
Tsutuo, T., Fujita, N. and Sato, S.

TITLE Method for controlling apoptosis and polypeptide controlling
JOURNAL Patient: WO 0215925-A 5 28-FEB-2002;

COMMENT KYOMA HAKKO KOGYO CO LTD, TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO

OS Homo sapiens (human)

PN WO 0215925-A/5

PD 28-FEB-2002

PR 22-AUG-2001 WO 2001JP007179

PI TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO

PC A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08,

PC A61P35/00, C07K7/04, C07K14/47, C07K16/18, C12N1/15, C12N1/19 PC

PC C12P21/02, C12N15/09, G01N33/50, G01N33/15, G01N33/566, G01N33/68

CC human AKt3

FT source Location/Qualifiers

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Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10

AY335691

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AY335691 1440 bp mRNA linear SYN 15-OCT-2003

Synthetic construct Homo sapiens v-act murine thymoma viral

oncogene-like 3 (AKT3) mRNA, partial cds.

AY335691.1 GI:33304020

FLI CDNA.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

other sequences; artificial sequences.

1 (bases 1 to 1440)

Park, J., Rolfe, A., Hu, Y., Shen, B., Vamberg, F., Moreira, D.,

Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.,

Labber, J., and Britzuela, L.

Cloning of human full-length CDS FLEXGene kinases in

recombinational vector system

Unpublished

2 (bases 1 to 1440)

Park, J., Rolfe, A., Hu, Y., Shen, B., Vamberg, F., Moreira, D.,

Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.,
LeBeet, J. and Brizuela, L.
Direct Submission
Submitted (02-JUL-2003) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141-2023, USA

COMMENT

This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
Each CDS has been cloned without stop-codon (to allow fusion with
C-terminal tag). The CDS has been directionally cloned using BD
In-Fusion(TM) cloning system between the SalI and HindIII sites of
the pDNR-Dual vector. Additional sequences in the clone: 'Acc'
after SalI site and before 'Atg' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame.

FEATURES

source

Location/Qualifiers
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gene

CDS

ORIGIN

Query Match 93.0%; Score 1438; DB 12; Length 1440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
BD251227
LOCUS BD251227 1436 bp DNA linear PAT 17-JUL-2003
DEFINITION Human Akt-3.
ACCESSION BD251227.1 GI:33060997
VERSION JP 2002535964-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1436)
AUTHORS Masure, S.L.J. and Richardson, A.
TITLE Human Akt-3
JOURNAL Patent: JP 2002535964-A 2 29-OCT-2002;
JANSSEN PHARMACEUTICA NV
COMMENT OS Homo sapiens (human)
PN JP 2002535964-A/2
PD 29-OCT-2002
PE 17-DEC-1999 JP 200589669
PR 22-DEC-1998 GB 9828375.7
PI STEFAN LEO JOZEF MASURE, ALAN RICHARDSON
PC C12N15/09, A61K31/713, A61K38/53, A61K39/395, A61K39/395, A61K48/00, PC
A61P35/00,
PC A61P43/00, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/
PC 12, C12Q1/02,
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CC Human Akt-3
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Best Local Similarity 99.9%; Pred. No. 2.4e-113;
Matches 1435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 181 TTATATATAACGAGACCAAGCAACCAACACTTTATATATCATGATGTCTCCAGTGCAT 240
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LOCUS AX026530 1436 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 2 from Patent WO0037613.
ACCESSION AK026530
VERSION AK026530.1 GI:10187718
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Maure, S.L. and Richardson, A.
TITLE Human akt-3
JOURNAL Patent: WO 0037613-A 2 29-JUN-2000;
MASUKE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
PHARMACEUTICA NV (BE)
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ORIGIN
Query Match 92.7%; Score 1434.4; DB 6; Length 1436;
Best Local Similarity 99.9%; Pred. No. 2,4e-313;
Matches 1435; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 ATGAGCGATGTTCCATTTGGAAGAAGGTTGGGTTCAAGAGGGGAGATATATATAA 70
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QY 71 AACTGAGGCCAGATACCTCTTTTGAAGAAGATGGCTCATTCATAGATATATAAG 130
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RESULT 13
BD250154
LOCUS 1570 bp DNA linear PAT 17-JUL-2003
DEFINITION AKT nucleic acids, polypeptides, and uses thereof.
ACCESSION BD250154
VERSION BD250154.1 GI:33059924
KEYWORDS JP 2002539781-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1570)
AUTHORS Guo, K., Pagnoni, M.F., Clark, K.L. and Ivaashchenko, Y.D.
TITLE AKT nucleic acids, polypeptides, and uses thereof
JOURNAL Patent: JP 2002539781-A 1 26-NOV-2002;
AVENTIS PHARMACEUTICALS PRODUCTS INC
OS Homo sapiens (human)
PN JP 2002539781-A/1
PD 26-NOV-2002
PF 14-MAR-2000 JP 2000606725
PI 19-MAR-1999 US 60/125108
C12N15/09, A61K9/127, A61K35/76, A61K38/00, A61K39/395, A61K47/36, PC
A61K47/42.

PC A61K47/46, A61K48/00, A61P1/16, A61P9/10, A61P13/12, A61P37/06, PC
A61P43/00,
PC C07K16/40, C12N1/19, C12N1/21, C12N5/10, C12N7/00, C12N9/12, C12Q1/
PC 48, G01N33/15,
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G01N33/50, G01N33/53, G01N33/56, (C12N1/19, C12R1:645), (C12N1/21, PC
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ORIGIN

Query Match 88.2%; Score 1364.8; DB 6; Length 1570;
Best Local Similarity 98.4%; Pred. No. 1.3e-297;
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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LOCUS AX056819
DEFINITION Sequence 1 from Patent WO0077190.
ACCESSION AX056819
VERSION AX056819.1 GI:12309760
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Guo, K., Ivashchenko, Y. and Clark, K.
Induction of vascular endothelial growth factor (vegf) by the
serine/threonine protein kinase akt
Patent: WO 0077190-A 1 21-DEC-2000;
JOURNAL Aventis Pharmaceuticals Inc. (US)
FEATURES
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ORIGIN

Query Match 88.2%; Score 1364.8; DB 6; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 1.3e-297;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 GGGAGTCATCATGAGCAGTGTACCATTTGTGAAAGAGTTGGGTTTCAGAAAGAGGAGAGA 60
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RESULT 15
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 LOCUS
 DEFINITION
 AX251592
 VERSION
 AX251592.1
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
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 AUTHORS
 Guo, K., Pagnoni, M.F., Clark, K.L. and Ivashchenko, Y.D.
 TITLE
 Akt nuclear acids, polypeptides, and uses thereof
 JOURNAL
 Patent: WO 0168850-A 1 20-SEP-2001;
 Aventis Pharmaceuticals Products Inc. (US)
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ORIGIN

PDJAKEIMRHSFSPGVNODVYDKLVPFKEQVTSSETDRYFDEBFTAQITITTPPE
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Query Match 88.2%; Score 1364.8; DB 6; Length 1570;
Best Local Similarity 98.4%; Pred. No. 1.3e-297;
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

QY 1 GGGAGCATCATGAGGATGTTACCATTTGGAAGAAGGTTGGGTTGAGAGGGGAGG 60
DB 116 GGGAGCATCATGAGGATGTTACCATTTGGAAGAAGGTTGGGTTGAGAGGGGAGG 175
QY 61 ATATATAAATACTGAGGCGCAAGATACCTCTTTTGAAGACAGATGCTCATTTCAATAG 120
DB 176 ATATATAAATACTGAGGCGCAAGATACCTCTTTTGAAGACAGATGCTCATTTCAATAG 235
QY 121 ATTTAAAGAGAACTTCAGATGTGATTTACCTTTACCTTCAACAATTTCAGTGGC 180
DB 236 ATTTAAAGAGAACTTCAGATGTGATTTACCTTTACCTTCAACAATTTCAGTGGC 295
QY 181 AAAATGCGAGTTATGTAAGAAACAGACGACCAAGCCAAACACATTTATATCAGATGCT 240
DB 296 AAAATGCGAGTTATGTAAGAAACAGACGACCAAGCCAAACACATTTATATCAGATGCT 355
QY 241 CCAAGTGAATCTGTTATAGAGAAACATTTCAATGATGATCTCCAGAGAAAGGAGAA 300
DB 356 CCAAGTGAATCTGTTATAGAGAAACATTTCAATGATGATCTCCAGAGAAAGGAGAA 415
QY 301 ATGAGACAGAGCTATCCAGGCTGTAGACAGACATGCGACAGGCAAGAAAGAGAGAT 360
DB 416 ATGAGACAGAGCTATCCAGGCTGTAGACAGACATGCGACAGGCAAGAAAGAGAGAT 475
QY 361 GAATGTAGTCAACTTCACAAATTTGATATATATAGAGAGAGAGATGATGCTCTAC 420
DB 476 GAATGTAGTCAACTTCACAAATTTGATATATATAGAGAGAGAGATGATGCTCTAC 535
QY 421 AACCCATCATTAAGAAAGCAATGATGATTTGATTTGAACTATAGTAAAG 480
DB 536 AACCCATCATTAAGAAAGCAATGATGATTTGATTTGAACTATAGTAAAG 595
QY 481 CACTTTTGGAAAGTTATTTTGGTTCGAGAGAGCAAGTGAATAATCTATGTAAG 540
DB 596 CACTTTTGGAAAGTTATTTTGGTTCGAGAGAGCAAGTGAATAATCTATGTAAG 655
QY 541 GATTCTGAAGAAAGTCAATTTTGCAGAGAGTGAAGTGGCACACACTTAACCTGAAG 600
DB 656 GATTCTGAAGAAAGTCAATTTTGCAGAGAGTGAAGTGGCACACACTTAACCTGAAG 715
QY 601 CAGAGTATTAAGAAACATAGACATCCCTTTTAACTCTTGAATAATCTCTTCAGAC 660
DB 716 CAGAGTATTAAGAAACATAGACATCCCTTTTAACTCTTGAATAATCTCTTCAGAC 775
QY 661 AAAAGACCGTTTGTGTTTGTGATGTAATGTTAATGGGGGAGAGCTGTTTCCATTT 720
DB 776 AAAAGACCGTTTGTGTTTGTGATGTAATGTTAATGGGGGAGAGCTGTTTCCATTT 835
QY 721 GTGAGAGAGCGGGTGTCTCTGAGAGCGCACACGTTTCTATGTGAGAAATGTCTC 780
DB 836 GTGAGAGAGCGGGTGTCTCTGAGAGCGCACACGTTTCTATGTGAGAAATGTCTC 895
QY 781 TGCCTTGACTATCTACATTCGCGAAAGATTTGTACCGTATCTCAAGTTGAGAAATCT 840
DB 896 TGCCTTGACTATCTACATTCGCGAAAGATTTGTACCGTATCTCAAGTTGAGAAATCT 955
QY 841 AATGCTGAGCAAAAGATGGCCACATTAATAATTAAGATTTTGAAGTTGCAAAAGAGGAT 900
DB 956 AATGCTGAGCAAAAGATGGCCACATTAATAATTAAGATTTTGAAGTTGCAAAAGAGGAT 1015
QY 901 CACAGATGACGACCACTGAGAAACATTTCTGAGCACTCCAGAAATCTGGCACCAAGGT 960
DB 1016 CACAGATGACGACCACTGAGAAACATTTCTGAGCACTCCAGAAATCTGGCACCAAGGT 1075
QY 961 GTTAGAAGATTAATGACTATGTCGAGCAGATGACTGTGTGGGCTTAGGGGTTGTCAATGTA 1020

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DB 1076 GTTAGAAGATTAATGACTATGTCGAGCAGATGACTGTGTGGGCTTAGGGGTTGTCAATGTA 1135
QY 1021 TGAATGATGATGAGAGGTTTACCTTTCTACAAACAGACCCATGAGAACTTTTGAAT 1080
DB 1136 TGAATGATGATGAGAGGTTTACCTTTCTACAAACAGACCCATGAGAACTTTTGAAT 1195
QY 1081 AATATTAATGAGAACATTAATAATTTCTGAGACACTCTCTTCAATGCAAAATCATTTGCT 1140
DB 1196 AATATTAATGAGAACATTAATAATTTCTGAGACACTCTCTTCAATGCAAAATCATTTGCT 1255
QY 1141 TTCAAGGCTCTTGATTAAGATCCAAATTAACGCTTTGTGAGAGACAGATGATGCAAA 1200
DB 1256 TTCAAGGCTCTTGATTAAGATCCAAATTAACGCTTTGTGAGAGACAGATGATGCAAA 1315
QY 1201 AGAATTAAGACACAGTTTCTCTGAGAGTAACTGGCAAGATGTTATGATTAATAA 1260
DB 1316 AGAATTAAGACACAGTTTCTCTGAGAGTAACTGGCAAGATGTTATGATTAATAA 1375
QY 1261 GCTTGACTCTCTTTTAACTCAAGTAAACATCTGAGACAGATGATGATGTA 1320
DB 1376 GCTTGACTCTCTTTTAACTCAAGTAAACATCTGAGACAGATGATGATGTA 1435
QY 1321 AGAATTAAGCTCAGACTATTAACAATAACCACTGAAATAATGATGAGATGTA 1380
DB 1436 AGAATTAAGCTCAGACTATTAACAATAACCACTGAAATAATGATGAGATGTA 1495
QY 1381 GGAATGCAATGACCAATGAGA 1400
DB 1496 TGGCATGCTGGGTAACTGGA 1515

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Search completed: April 13, 2005, 06:12:26
Job time : 6629 secs

KM human; serine/threonine kinase Akt-3; chromosome 1; gene; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 11.1450
 FT CDS /tag= a
 FT /product= "serine/threonine kinase Akt-3"
 XX
 PN WO2004041185-A2.
 XX
 PD 21-MAY-2004.
 XX
 PP 31-OCT-2003; 2003WO-US034636.
 XX
 PR 31-OCT-2002; 2002US-0423340P.
 XX
 PA (UVRP) UNIV ROCHESTER.
 XX
 PI Chang C, Lee Y, Lin W;
 XX
 DR WPI; 2004-390508/36.
 DR P-PSDB; ADN71940.
 XX
 PT Composition useful in the treatment of e.g. prostate cancer comprises a
 PT kinase pathway inhibitor and an anti-prostate cancer compound.
 XX
 PS Disclosure; SEQ ID NO 25; 118pp; English.
 XX
 CC The present invention describes a composition (C1) which comprises a
 CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
 CC Also described: (1) identification of a mitogen-activated protein (MAP)
 CC kinase pathway inhibitor involving incubating an androgen or a
 CC library of molecules with a cell containing an activable MAP kinase
 CC pathway and selecting the molecules which inhibit the activation of the
 CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
 CC involving incubating a cell with hydroxyflutamide and potential
 CC inhibitor, and assaying the level of activation of MAP kinase pathway or
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
 CC cytosolic activity, and can be used as a MAP kinase inhibitor,
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
 CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
 CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
 CC prostate cancer inhibitor; and for reducing the number of prostate cancer
 CC cells in a sample. The composition C1 provides effective combination
 CC therapy as compared to prior therapies. The present sequence encodes
 CC human serine/threonine kinase Akt-3, which is used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1547; DB 12; Length 1547;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 CCAAGTGAAGTCTGTTATAGAGAAACATTTCATGTAGTACTCCAGAGAAAGGAGAGA 300
 QY
 Db 301 ATGACAGAAAGCTATTCAGGCTGTAGCAGACGACTGCAGAGCCAAAGAGAGAGAT 360
 QY
 Db 301 ATGACAGAAAGCTATTCAGGCTGTAGCAGACGACTGCAGAGCCAAAGAGAGAGAT 360
 QY
 Db 361 GAATGTAGTCCAACTTCAAAATTGATTAATAGAGAGAAAGATGATGCTCTAC 420
 QY
 Db 361 GAATGTAGTCCAACTTCAAAATTGATTAATAGAGAGAAAGATGATGCTCTAC 420
 QY
 Db 421 AACCATCATTAAGAAAGAAACAATGATGATTTGATTAATTTGAACTACTAGTAAAG 480
 QY
 Db 421 AACCATCATTAAGAAAGAAACAATGATGATTTGATTAATTTGAACTACTAGTAAAG 480
 QY
 Db 481 CACTTTGGGAAAGTTATTTGGTTGAGAGAAAGGCAAGTGGAAATATATGCTATGAA 540
 QY
 Db 481 CACTTTGGGAAAGTTATTTGGTTGAGAGAAAGGCAAGTGGAAATATATGCTATGAA 540
 QY
 Db 541 GATTCTGAAGAAAGAAAGTATTTGCAAAAGATGAGTGAAGGACACTCTAAGTGAAG 600
 QY
 Db 541 GATTCTGAAGAAAGAAAGTATTTGCAAAAGATGAGTGAAGGACACTCTAAGTGAAG 600
 QY
 Db 601 CAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATCTCTCCAGAC 660
 QY
 Db 601 CAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATCTCTCCAGAC 660
 QY
 Db 661 AAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTCCATT 720
 QY
 Db 661 AAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTCCATT 720
 QY
 Db 721 GTCCGAGAGGCGGGGTGTTCTGAGGACCGCACAGTTTCTAATGGGCAAAATTTCTC 780
 QY
 Db 721 GTCCGAGAGGCGGGGTGTTCTGAGGACCGCACAGTTTCTAATGGGCAAAATTTCTC 780
 QY
 Db 781 TGCCTTGAAGCTATCTACATTTCCGGAAGATGTGATCGTGAATCTCAAGTGAAGATCT 840
 QY
 Db 781 TGCCTTGAAGCTATCTACATTTCCGGAAGATGTGATCGTGAATCTCAAGTGAAGATCT 840
 QY
 Db 841 AATGCTGCAAAAGATGCGCACATTAATAATTCAGATTTTGAATTTGCAAAAGAGGAT 900
 QY
 Db 841 AATGCTGCAAAAGATGCGCACATTAATAATTCAGATTTTGAATTTGCAAAAGAGGAT 900
 QY
 Db 901 CACAGATGAGGACACATGAAAGCAATTCGTGAGCACTCCAGAAATCTGGCCACGAGGT 960
 QY
 Db 901 CACAGATGAGGACACATGAAAGCAATTCGTGAGCACTCCAGAAATCTGGCCACGAGGT 960
 QY
 Db 961 GTTAGAAGATTAATGACTATGAGCGGAGAGTAGTGTGAGGCTTATGAGGCTTCAATGTA 1020
 QY
 Db 961 GTTAGAAGATTAATGACTATGAGCGGAGAGTAGTGTGAGGCTTATGAGGCTTCAATGTA 1020
 QY
 Db 961 GTTAGAAGATTAATGACTATGAGCGGAGAGTAGTGTGAGGCTTATGAGGCTTCAATGTA 1020
 QY
 Db 1021 TGAATGATGTGTGGAGGTTAATCTTTCTTACACACAGACCAATGAGAAATCTTTGAATT 1080
 QY
 Db 1021 TGAATGATGTGTGGAGGTTAATCTTTCTTACACACAGACCAATGAGAAATCTTTGAATT 1080
 QY
 Db 1081 AATATTAATGAAGAAACATTAATTTCTCGAACAATCTCTTCAAGATGCAAAATCATGTCT 1140
 QY
 Db 1081 AATATTAATGAAGAAACATTAATTTCTCGAACAATCTCTTCAAGATGCAAAATCATGTCT 1140
 QY
 Db 1141 TTCAGGCTCTTGAATTAAGATCCAAATTAAGCGCTTGTGAGAGACAGATGATGCAAA 1200
 QY
 Db 1141 TTCAGGCTCTTGAATTAAGATCCAAATTAAGCGCTTGTGAGAGACAGATGATGCAAA 1200
 QY
 Db 1201 AGAAATTAAGACACAGTTTCTTCTGAGATTAATCTGGCAAGATGTATGATTAATAA 1260
 QY
 Db 1201 AGAAATTAAGACACAGTTTCTTCTGAGATTAATCTGGCAAGATGTATGATTAATAA 1260
 QY
 Db 1261 GCTTGTACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTGAATGA 1320
 QY
 Db 1261 GCTTGTACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTGAATGA 1320
 QY
 Db 1321 AGAATTTACAGCTCAGACTATTAACAATTAACAACCTGAAAATATGATGAGAGATGTAT 1380
 QY
 Db 1321 AGAATTTACAGCTCAGACTATTAACAATTAACAACCTGAAAATATGATGAGAGATGTAT 1380


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Db      1245 TGCCTTGACTATCTACATTCCGAAAAGATGTGTACCGTATCTCAAGTTGGAGATCT 1304
Qy      841 AATGCTGACAAAGATGGCCACATTAATAATTAAGATTTTGGACTTTGGCAAGAAGGAT 900
Db      1305 AATGCTGACAAAGATGGCCACATTAATAATTAAGATTTTGGACTTTGGCAAGAAGGAT 1364
Qy      901 CACAGATGACCCACCATGAAAGACATTTCTGTGGCACTCCAGAAATCTGGCACCAGAGT 960
Db      1365 CACAGATGACCCACCATGAAAGACATTTCTGTGGCACTCCAGAAATCTGGCACCAGAGT 1424
Qy      961 GTTAGAAGATATGACTATATGCGCAGACAGTAGATGTGTGGGCTTATGATGTA 1020
Db      1425 GTTAGAAGATATGACTATATGCGCAGACAGTAGATGTGTGGGCTTATGATGTA 1484
Qy      1021 TGAATATGATGTGTGGAGGTTACTTTCTTACAAACAGAGACATGAGAAATTTTGAATT 1080
Db      1485 TGAATATGATGTGTGGAGGTTACTTTCTTACAAACAGAGACATGAGAAATTTTGAATT 1544
Qy      1081 AATATTTATGGAAGACATTAATTTCTGTGACACATCTTTCAGATGCAAAATCATTTGCT 1140
Db      1545 AATATTTATGGAAGACATTAATTTCTGTGACACATCTTTCAGATGCAAAATCATTTGCT 1604
Qy      1141 TTCAGGGCTCTTGATTAAGGATCCAAATAAACGCTTGTGTGAGACACAGATGATGCATA 1200
Db      1605 TTCAGGGCTCTTGATTAAGGATCCAAATAAACGCTTGTGTGAGACACAGATGATGCATA 1664
Qy      1201 AGAATTTATGAGACACAGTTTCTTCTGTGAGTAACTGGCAAGATGTATATATATAAA 1260
Db      1665 AGAATTTATGAGACACAGTTTCTTCTGTGAGTAACTGGCAAGATGTATATATATAAA 1724
Qy      1261 GCTTGACCTCCCTTTTAAACCTCAAGTAACATCTGAGACAGATCAATGATTTTATATA 1320
Db      1725 GCTTGACCTCCCTTTTAAACCTCAAGTAACATCTGAGACAGATCAATGATTTTATATA 1784
Qy      1321 AGAATTTATGAGCTCAGACTATTAACAATAACACCCTGTAATAATGATGAGATGATAT 1380
Db      1785 AGAATTTATGAGCTCAGACTATTAACAATAACACCCTGTAATAATGATGAGATGATAT 1844
Qy      1381 GGAATGATGAGACAAATGAGAGGGGGCGCATTTTCCCTCAATTTTCTTACTCTGCAAGTGG 1440
Db      1845 GGAATGATGAGACAAATGAGAGGGGGCGCATTTTCCCTCAATTTTCTTACTCTGCAAGTGG 1904
Qy      1441 ACAGAGATAGATCTCTTTCATCTGCACTGCACTGCACTTCAATTTATTTACTGAAAA 1500
Db      1905 ACAGAGATAGATCTCTTTCATCTGCACTGCACTGCACTTCAATTTATTTACTGAAAA 1964
Qy      1501 TGAATCTGAGACATCAACAATCTTACTTACATAGCAGAGGGA 1547
Db      1965 TGAATCTGAGACATCAACAATCTTACTTACATAGCAGAGGGA 2011

RESULT 4
AAC61592
ID      AAC61592 standard; DNA; 2367 BP.
XX
AC      AAC61592;
XX
DT      19-FEB-2001 (first entry)
XX
DE      DNA encoding a human kinase B-gamma polypeptide.
XX
KM      Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;
KW      phosphoinositide 3-kinase; insulin signalling;
KW      pleckstrin homology domain; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      10..1449
FT      /tag= a
FT      /product= "kinase B-gamma polypeptide"
XX
PN      MO200058446-A1.
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XX      05-OCT-2000.
PD      23-MAR-2000; 2000MO-SE000571.
XX      25-MAR-1999; 99SE-00001115.
PR      (PMAA ) PHARMACIA & UPJOHN AB.
XX
PI      Altersand A;
DR      WPI; 2000-647230/62.
DR      P-PSDB; AAB19284.
XX
PT      Novel human protein kinase B gamma polynucleotides and polypeptides
PT      useful as probe or primers in polymerase chain reaction and to raise
PT      antibodies useful in diagnostic assays for detecting polypeptide
PT      expression.
XX
PS      Claim 1; Page 16-19; 27pp; English.
XX
CC      The present sequence encodes a human protein kinase B gamma (PKB)
CC      polypeptide. PKB is activated by insulin or insulin growth factor 1.
CC      lipid products of phosphoinositide 3-kinase act in insulin signalling by
CC      binding to pleckstrin homology domains of PKB. PKB polynucleotides may be
CC      used as a source of probes and primers. PKB polypeptides are used to
CC      raise antibodies, which are used in diagnostic assays. The polypeptides
CC      are also useful for screening for compounds which affect insulin
CC      signalling pathways
XX
SO      Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 U; 0 Other;

Query Match      99.8%; Score 1544.4; DB 3; Length 2367;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGAATGATGAGAGGATGTTTCAATTTGAAAGAAAGTTGGGTTGAGAGAGGAGAA 61
Db      1 GGAATGATGAGAGGATGTTTCAATTTGAAAGAAAGTTGGGTTGAGAGAGGAGAA 60
Qy      62 TATATTAAGAAAGCTGAGGCAAGATATCTCTTTGGAAGACAGATGCTCATTCATAGGA 121
Db      61 TATATTAAGAAAGCTGAGGCAAGATATCTCTTTGGAAGACAGATGCTCATTCATAGGA 120
Qy      122 TATTAAGAAAGAACTCAAGATGATGATTTACTTATCCCTCAACAACCTTTTCAAGTGGCA 181
Db      121 TATTAAGAAAGAACTCAAGATGATGATTTACTTATCCCTCAACAACCTTTTCAAGTGGCA 180
Qy      182 AATATGCAATTAATGAAACAGAAAGCAAGGCAAAACATTTATATGAGATGTC 241
Db      181 AATATGCAATTAATGAAACAGAAAGCAAGGCAAAACATTTATATGAGATGTC 240
Qy      242 CAGTGACTACTGTTATAGAGAAACATTTCAATGATATCTCCAGAGAAAGGAAAGAA 301
Db      241 CAGTGACTACTGTTATAGAGAAACATTTCAATGATATCTCCAGAGAAAGGAAAGAA 300
Qy      302 TGAACAGAAAGCTATCCAGGCTGTATGACAGACAGCTGACAGAGCAAGAGAGAGATG 361
Db      301 TGAACAGAAAGCTATCCAGGCTGTATGACAGACAGCTGACAGAGCAAGAGAGAGATG 360
Qy      362 AATTTGATGCCAATTCACAATTTGATATATATGAGAGAGAGAGATGATGCTCTTACA 421
Db      361 AATTTGATGCCAATTCACAATTTGATATATATGAGAGAGAGAGATGATGCTCTTACA 420
Qy      422 ACCATCATTAAGAAAGCAATGATGATTTTGAATTTGAACTATTTGAACTAAGTAAGGC 481
Db      421 ACCATCATTAAGAAAGCAATGATGATTTTGAATTTGAACTAAGTAAGTAAGGC 480
Qy      482 ACTTTTGGGAAAGTTATTTTGTGTGAGAGAGCAAGTGAAGTAATATCTATCTATGAAG 541
Db      481 ACTTTTGGGAAAGTTATTTTGTGTGAGAGAGCAAGTGAAGTAATATCTATCTATGAAG 540
Qy      542 ATTTCGAAGAAAGAGTCAATTATTTGCAAGAGATGAAGTGGCAACACTTAATGAAAGC 601
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Db      ||||||| 541 ATTCTGAAGAAAGAGTCATTAATGCAAGATGAAGTGGACACACTCTAATCTGAAAGC 600
Qy      ||||||| 602 AAGATTTAAAGAACCTAGACATCCCTTTTAAACATCCTTAAATATCTCTCCAGACA 661
Db      ||||||| 601 AAGATTTAAAGAACCTAGACATCCCTTTTAAACATCCTTAAATATCTCTCCAGACA 660
Qy      ||||||| 662 AAAGACCGTTTGTGTTTGTGATGAAATGTTAAATGGGGGAGAGCTGTTTCCATTGG 721
Db      ||||||| 661 AAAGACCGTTTGTGTTTGTGATGAAATGTTAAATGGGGGAGAGCTGTTTCCATTGG 720
Qy      ||||||| 722 TCGAAGAGACGGGAGTCTCTGAGAGACCGACACGTTTCTATGTGTGACAGAAATGTCTCT 781
Db      ||||||| 721 TCGAAGAGACGGGAGTCTCTGAGAGACCGACACGTTTCTATGTGTGACAGAAATGTCTCT 780
Qy      ||||||| 782 GCGTTGAGATCTATCTATCCCGGAAAAGATGTGTATCCCGATCTCAAGTGTGAGATCTTA 841
Db      ||||||| 781 GCGTTGAGATCTATCTATCCCGGAAAAGATGTGTATCCCGATCTCAAGTGTGAGATCTTA 840
Qy      ||||||| 842 ATGCTGACAAAGATGCGCCACATTAATTAAGATTTTGAATTGCAATTTGGCAAGAGGATC 901
Db      ||||||| 841 ATGCTGACAAAGATGCGCCACATTAATTAAGATTTTGAATTGCAATTTGGCAAGAGGATC 900
Qy      ||||||| 902 ACAGATGACGCCACCATGAAAGACATTTGTGSCACTCCAGAAATATCTGGCACAGAGTG 961
Db      ||||||| 901 ACAGATGACGCCACCATGAAAGACATTTGTGSCACTCCAGAAATATCTGGCACAGAGTG 960
Qy      ||||||| 962 TTAGAAGATTAATGACATATGCGGAGACATGAGTGTGGGGCTGAGGGTCTCATGAT 1021
Db      ||||||| 961 TTAGAAGATTAATGACATATGCGGAGACATGAGTGTGGGGCTGAGGGTCTCATGAT 1020
Qy      ||||||| 1022 GAATGATGTGTGGAGGTTACCTTCTCAACACAGACCATGAGAACTTTTGAATTA 1081
Db      ||||||| 1021 GAATGATGTGTGGAGGTTACCTTCTCAACACAGACCATGAGAACTTTTGAATTA 1080
Qy      ||||||| 1082 AATTTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTT 1141
Db      ||||||| 1081 AATTTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTT 1140
Qy      ||||||| 1142 TCAGGGCTCTGATTAAGATGCAAAATTAAGCCCTTGTGGAGGACCAAGATATGCAAAA 1201
Db      ||||||| 1141 TCAGGGCTCTGATTAAGATGCAAAATTAAGCCCTTGTGGAGGACCAAGATATGCAAAA 1200
Qy      ||||||| 1202 GAATTTATGAGACACAGTTTCTCTCTGAGTAACTGGCAAGATGATATGATAAAG 1261
Db      ||||||| 1201 GAATTTATGAGACACAGTTTCTCTCTGAGTAACTGGCAAGATGATATGATAAAG 1260
Qy      ||||||| 1262 CTGTGACCTCTTTTAAACCTCAAGTACATCTGAGACAGATACTAGATATTTGATGA 1321
Db      ||||||| 1261 CTGTGACCTCTTTTAAACCTCAAGTACATCTGAGACAGATACTAGATATTTGATGA 1320
Qy      ||||||| 1322 GAATTTAAGCTCAGACTATTTAACAATTAACACACCTGAAATAATGATGAGATGTAG 1381
Db      ||||||| 1321 GAATTTAAGCTCAGACTATTTAACAATTAACACACCTGAAATAATGATGAGATGTAG 1380
Qy      ||||||| 1382 GACTCATGAGCAATGAGAGGCGGCAGATTTCCCTCAATTTTCTACTCTCAAGTGA 1441
Db      ||||||| 1381 GACTCATGAGCAATGAGAGGCGGCAGATTTCCCTCAATTTTCTACTCTCAAGTGA 1440
Qy      ||||||| 1442 CGAAGATAAGTCTCTTCAATCTGCTACTTCACTGATCTTCAATTTATTAATGAAT 1501
Db      ||||||| 1441 CGAAGATAAGTCTCTTCAATCTGCTACTTCACTGATCTTCAATTTATTAATGAAT 1500
Qy      ||||||| 1502 GATTCCTGAGACATCACCACTAGCTTACATCAACATGAGAGGGGCA 1547
Db      ||||||| 1501 GATTCCTGAGACATCACCACTAGCTTACATCAACATGAGAGGGGCA 1546

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RESULT 5
ADCC26888
ID ADCC26888 standard; DNA; 2811 BP.
XX
AC ADCC26888;

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XX      18-DEC-2003 (first entry)
DT      DNA encoding human Akt3.
XX      de; gene; Akt; human; apoptosis; myocardial infarction;
KW      hyperproliferative disease; cancer; rheumatoid arthritis;
KW      inflammatory bowel disease; osteoarthritis; leiomyoma; adenoma; lipoma;
KW      haemangioma; fibroma; vascular occlusion; restenosis; atherosclerosis;
KW      pre-neoplastic lesion; adenomatous hyperplasia;
KW      prostatic intraepithelial neoplasia; carcinoma in situ;
KW      oral hairy leukoplakia; psoriasis.
XX      Homo sapiens.
XX      US2003144204-A1.
XX      31-JUL-2003.
XX      19-DEC-2002; 2002US-00324985.
XX      19-DEC-2001; 2001US-0342155P.
XX      (BAYU ) BAYLOR COLLEGE MEDICINE.
XX      Spencer D;
XX      WPI; 2003-720709/68.
XX      New expression vector for modulating apoptosis or for treating myocardial
PT      infarction or cancer, comprises an inducible chimeric protein that
PT      comprises a mutant Akt polypeptide fused to a ligand-binding domain.
XX      Disclosure; SEQ ID NO 4; 38bp; English.
XX      The invention relates to an expression vector comprising an inducible
CC      chimeric protein which comprises a mutant Akt polypeptide fused to a
CC      ligand-binding domain. The composition and methods are useful in
CC      modulating apoptosis or in treating myocardial infarction or
CC      hyperproliferative diseases such as cancer, rheumatoid arthritis,
CC      inflammatory bowel disease, osteoarthritis, leiomyoma, adenoma,
CC      lipomas, haemangiomas, fibromas, vascular occlusion, restenosis,
CC      atherosclerosis, pre-neoplastic lesions (e.g. adenomatous hyperplasia or
CC      prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy
CC      leukoplakia or psoriasis. The present sequence represents DNA encoding
CC      human Akt3.
XX      SQ
XX      Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;
XX      Query Match 99.4%; Score 1537; DB 10; Length 2811;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 ATGACGATGTTACCATTTGTGAAGAGTTGGTTCAAGAGGGGCAATATATTA 70
Db      1 ATGACGATGTTACCATTTGTGAAGAGTTGGTTCAAGAGGGGCAATATATTA 60
Qy      71 AACTGAGGCCAAGTACTCTCTTTGAAGACAGATGCTCATTTATGATATTAAG 130
Db      71 AACTGAGGCCAAGTACTCTCTTTGAAGACAGATGCTCATTTATGATATTAAG 120
Qy      131 AAACCTCAAGATGATGATTTACCTTATCCCTCAACAATTTTCTAGTGGCAAAATGCCAG 190
Db      131 AAACCTCAAGATGATGATTTACCTTATCCCTCAACAATTTTCTAGTGGCAAAATGCCAG 180
Qy      191 TTAATGAAGAACGAAACGACCAAGCCAAACATTTATATGATGTCTCCAGTGA 250
Db      181 TTAATGAAGAACGAAACGACCAAGCCAAACATTTATATGATGTCTCCAGTGA 240
Qy      251 ACTGTTATAGAGAGAACATTTTCAATGATATCTCCAGAGGAAAGGAATGACAGAA 310
Db      241 ACTGTTATAGAGAGAACATTTTCAATGATATCTCCAGAGGAAAGGAATGACAGAA 300

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CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidemia,
CC dyslipidemia, high blood pressure or heart failure. As such, they
CC exhibit cardiant, thrombolytic, anticoagulant, antilipemic, hypotensive
CC and cardiant activities. This polynucleotide sequence is a human DNA
CC molecule that is differentially expressed in a patient with a
CC cardiovascular disorder, given in an exemplification of the invention.

XX Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;

Query Match 99.4%; Score 1537; DB 13; Length 2811;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ATGAGCGATGTTACCATGTTGAAGAGGTTGGGTTCAAGAGGGGAGATATATATAA 70
DB 1 ATGAGCGATGTTACCATGTTGAAGAGGTTGGGTTCAAGAGGGGAGATATATATAA 60
QY 71 AACTGAGGCCAAGATATCTCTTTTGAAGACAGATGCTCATTTAGATATATAAG 130
DB 61 AACTGAGGCCAAGATATCTCTTTTGAAGACAGATGCTCATTTAGATATATAAG 120
QY 131 AAACCTCAAGATGATGATTTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCCG 190
DB 121 AAACCTCAAGATGATGATTTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCCG 180
QY 191 TTAATGAAGACAGACCAAGCAAAACATTTATATATAGATGTCCTCAGTGGACT 250
DB 181 TTAATGAAGACAGACCAAGCAAAACATTTATATATAGATGTCCTCAGTGGACT 240
QY 251 ACTGTTATAGAGAACATTTCTATGATATCTCCAGAGAAAGGAGATATGACAGAA 310
DB 241 ACTGTTATAGAGAACATTTCTATGATATCTCCAGAGAAAGGAGATATGACAGAA 300
QY 311 GCTATTCAGGCTGTAGACAGACCTGCAAGGCAAGAAAGAGAGATGATTTAGT 370
DB 301 GCTATTCAGGCTGTAGACAGACCTGCAAGGCAAGAAAGAGAGATGATTTAGT 360
QY 371 CCAACTTCAAAATTTATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 430
DB 361 CCAACTTCAAAATTTATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 420
QY 431 AAAAGAGACATGATGATTTTGAATTTGAAATCTAAGTAAAGGCACTTTTGGG 490
DB 421 AAAAGAGACATGATGATTTTGAATTTGAAATCTAAGTAAAGGCACTTTTGGG 480
QY 491 AAAAGTATTTTGGTTGAGAGAAAGGCAAGTGAATAATCTATGATTTCTGAAG 550
DB 481 AAAAGTATTTTGGTTGAGAGAAAGGCAAGTGAATAATCTATGATTTCTGAAG 540
QY 551 AAAAGAGTATTTTGAAGAGTGAAGTGGGCAACACTCTAAGTGAAGAGATATTA 610
DB 541 AAAAGAGTATTTTGAAGAGTGAAGTGGGCAACACTCTAAGTGAAGAGATATTA 600
QY 611 AAGAACATGACATCCCTTTTAACTCTTGAATAATCTCTTCCAGCAAAAGACGT 670
DB 601 AAGAACATGACATCCCTTTTAACTCTTGAATAATCTCTTCCAGCAAAAGACGT 660
QY 671 TTGTGTTTGTGATGGAATATGTTAATGGGGGAGACTGTTTTCATTTGTCGAGAG 730
DB 661 TTGTGTTTGTGATGGAATATGTTAATGGGGGAGACTGTTTTCATTTGTCGAGAG 720
QY 731 CGGGTGTCTGAGAGACGCGACAGCTTTCTAATGTCGAGAAATGTCCTGCTGGAC 790
DB 721 CGGGTGTCTGAGAGACGCGACAGCTTTCTAATGTCGAGAAATGTCCTGCTGGAC 780
QY 791 TATCTACATTCGGAAGATTTGTATCGTATCTCAAGTGGAGAAATCTAAATGCTGGAC 850

DB 781 TATCTACATTCGGAAGATTTGTATCGTATCTCAAGTGGAGAAATCTAAATGCTGGAC 840
QY 851 AAAAGTGGCCACATATAAATTTACATATTTTGGACTTTTCCAAAGAGATCACATGCA 910
DB 841 AAAAGTGGCCACATATAAATTTACATATTTTGGACTTTTCCAAAGAGATCACATGCA 900
QY 911 GCCACCATGAAGACATTCCTGTGGCACTCCAGAAATTTGCGCACGAGAGTGTAAAGAT 970
DB 901 GCCACCATGAAGACATTCCTGTGGCACTCCAGAAATTTGCGCACGAGAGTGTAAAGAT 960
QY 971 AATGACTATGCGCGAGCAGTATGATGTTGGGGCTTGAAGGATTTGATGAAATGATG 1030
DB 961 AATGACTATGCGCGAGCAGTATGATGTTGGGGCTTGAAGGATTTGATGAAATGATG 1020
QY 1031 TGTGGAGGTTACCTTTCTACACACAGACCAATGTAAGATTTTGAATTAATTAATG 1090
DB 1021 TGTGGAGGTTACCTTTCTACACACAGACCAATGTAAGATTTTGAATTAATTAATG 1080
QY 1091 GAAGACATTTAATTTCTCTGCAACACTCTCTTCAATGCAAAATCATTCCTTCAAGGCTC 1150
DB 1081 GAAGACATTTAATTTCTCTGCAACACTCTCTTCAATGCAAAATCATTCCTTCAAGGCTC 1140
QY 1151 TTGATTAAGAGATCCAAATTAACGCTTGTGTGAGAGACCAAGATGATCAAAAGAAATATG 1210
DB 1141 TTGATTAAGAGATCCAAATTAACGCTTGTGTGAGAGACCAAGATGATCAAAAGAAATATG 1200
QY 1211 AGACACAGTTCTCTCTGAGATAACCTGCAAGATGATTAATTAAGATTTTACCT 1270
DB 1201 AGACACAGTTCTCTCTGAGATAACCTGCAAGATGATTAATTAAGATTTTACCT 1260
QY 1271 CCTTTTAAACCTCAAGTAAATCTGAGACAGATCTAGATATTTTGAAGAAATTTTACA 1330
DB 1261 CCTTTTAAACCTCAAGTAAATCTGAGACAGATCTAGATATTTTGAAGAAATTTTACA 1320
QY 1331 GCTCAGACTATTTACAATAACACACCTGAAATAATATGATGATGATGATGATG 1390
DB 1321 GCTCAGACTATTTACAATAACACACCTGAAATAATATGATGATGATGATGATG 1380
QY 1391 GACAAATGAGAGGCGGCGCATTTCCCTCAATTTTCTCTGCAAGTGGAGCAAGATTA 1450
DB 1381 GACAAATGAGAGGCGGCGCATTTCCCTCAATTTTCTCTGCAAGTGGAGCAAGATTA 1440
QY 1451 GTCTCTTCAATTCCTCTACTTCACTGATCATCTTCAATTTATTAAGTAAATGCTGG 1510
DB 1441 GTCTCTTCAATTCCTCTACTTCACTGATCATCTTCAATTTATTAAGTAAATGCTGG 1500
QY 1511 ACATCAACAGTCTTACCTTTACATAGACAGAGGCA 1547
DB 1501 ACATCAACAGTCTTACCTTTACATAGACAGAGGCA 1537

RESULT 7
AA62451
ID AAA62451 standard; cDNA; 1440 BP.
XX
XX AAA62451;
DT 13-NOV-2000 (first entry)
XX
XX Human Akt-3 coding sequence.
KW Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytosolic;
KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
KW Chromosome 1q43-44; 88.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1440
FT /*tag= a
FT /product= "Akt-3"
XX

PN WO200037613-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-GB004311.
 XX
 PR 22-DEC-1998; 98GB-00028375.
 XX
 PA (JANC) JANSSEN PHARM NV.
 PI Measure SLJ, Richardson A;
 XX
 DR WPI; 2000-498840/44.
 DR P-PSDB; AAB13393.
 XX
 PT New human serine/threonine kinase protein and the polynucleotide encoding
 PT the protein, useful for preparing a medicament for treating disorders
 PT associated with human serine/threonine kinase protein activity,
 PT especially cancer.
 XX
 PS Claim 4; Fig 1; 61pp; English.
 XX
 CC The present sequence is the coding region of the nucleotide sequence that
 CC encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also
 CC known as protein kinase B (PKB) or "related to A and C protein kinase"
 CC (RAC-PK). The gene encoding Akt-3 is located on human chromosome 1,
 CC region q43-q44. A human hippocampal EST sequence that showed high
 CC similarity to the rat RAC-Pygamma sequence was used to design primers for
 CC 3' rapid amplification of cDNA ends (3' RACE). The sequence obtained in
 CC the first round of 3' RACE was used to design primers for a second round.
 CC The complete sequence was then amplified from human hippocampal cDNA by
 CC PCR using primers based on the product of the second round of 3' RACE.
 CC Akt can inhibit apoptosis induced by detachment from the extracellular
 CC matrix. The Akt-3 nucleic acid molecule and protein may be used as
 CC medicaments for treating cancer. Agents which influence the activity of
 CC Akt-3 protein, and so stimulate apoptosis, may also be used to treat
 CC diseases associated with Akt-3
 XX
 SO Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Query Match 93.1%; Score 1440; DB 3; Length 1440;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ATGAGGATGTTACCAATGTGAAAGAGTGGCTCAGAAAGGGGAGAAATATATATAA 70
 DB 1 ATGAGGATGTTACCAATGTGAAAGAGTGGCTCAGAAAGGGGAGAAATATATATAA 60
 QY 71 AACTGAGGCCAGATACCTTCTTGAAAGACAGATGGCTCATTCATAGATATATAAG 130
 DB 61 AACTGAGGCCAGATACCTTCTTGAAAGACAGATGGCTCATTCATAGATATATAAG 120
 QY 131 AAACCTCAAGATGATGATTTTACCTTATCCCTCAACAACCTTTCACTGGCAAAATGCCAG 190
 DB 121 AAACCTCAAGATGATGATTTTACCTTATCCCTCAACAACCTTTCACTGGCAAAATGCCAG 180
 QY 191 TTATATGAAAACAGACGACCAAGCCAAACACATTTATATCAAGATGTCTCCAGTGA 250
 DB 181 TTATATGAAAACAGACGACCAAGCCAAACACATTTATATCAAGATGTCTCCAGTGA 240
 QY 251 AACTGATATGAGAGCACTTCTGATAGATCCGAGAGAAAGGAAAGATGAGACGAA 310
 DB 241 AACTGATATGAGAGCACTTCTGATAGATCCGAGAGAAAGGAAAGATGAGACGAA 300
 QY 311 GGTATCAGGCTGTAGACAGACACTGACAGAGCCAAAGAGAGAGAGATGATTTAGT 370
 DB 301 GGTATCAGGCTGTAGACAGACACTGACAGAGCCAAAGAGAGAGAGATGATTTAGT 360
 QY 371 CCAACTTCACAAATTTGATATATAGAGAGAAAGATGATGATCTCTACACCATCAT 430
 DB 361 CCAACTTCACAAATTTGATATATAGAGAGAGATGATGATCTCTACACCATCAT 420
 QY 431 AAAAGAAAGACATGATGATTTTGAATTTTGAATCTAGTAAAGCACTTTTGGG 490

DB 421 AAAAGAAAGACATGATGATTTTGAATTTTGAATCTAGTAAAGCACTTTTGGG 480
 QY 491 AAAATTATTTTGGTTCGAGAGAAAGGCAAGTGAAAAATCTATGCTATGAAATTTGAA 550
 DB 481 AAAATTATTTTGGTTCGAGAGAAAGGCAAGTGAAAAATCTATGCTATGAAATTTGAA 540
 QY 551 AAAAGATGATATTTGCAAAAGATGAGATGGGCAACACTCTAATGAAAGCAAGATTA 610
 DB 541 AAAAGATGATATTTGCAAAAGATGAGATGGGCAACACTCTAATGAAAGCAAGATTA 600
 QY 611 AAGAACATGACATCCCTTTTAAACATCCCTTGAATATTTCTCCAGCAAAAAGCCGT 670
 DB 601 AAGAACATGACATCCCTTTTAAACATCCCTTGAATATTTCTCCAGCAAAAAGCCGT 660
 QY 671 TTGTGTTTTGTATGATGATATATGTTAAATGAGGAGCTGTCTTTTCAATTTGCGAGAG 730
 DB 661 TTGTGTTTTGTATGATGATATATGTTAAATGAGGAGCTGTCTTTTCAATTTGCGAGAG 720
 QY 731 CCGGTGTTCTGTGAGACCGGACACGTTCTATGTGCGAGAAATGTCTCTGCTTGAC 790
 DB 721 CCGGTGTTCTGTGAGACCGGACACGTTCTATGTGCGAGAAATGTCTCTGCTTGAC 780
 QY 791 TATCTACATTCGGAAGAAAGTGTGACGCGATCTCAAGTTGGAGAAATCTTAATGCTGAC 850
 DB 781 TATCTACATTCGGAAGAAAGTGTGACGCGATCTCAAGTTGGAGAAATCTTAATGCTGAC 840
 QY 851 AAAGATGGCCACATTAATAATTCAGATTTTGAATTTGCAATTTGCAAGAAAGGATCA 910
 DB 841 AAAGATGGCCACATTAATAATTCAGATTTTGAATTTGCAATTTGCAAGAAAGGATCA 900
 QY 911 GCCACATGAAAGCATTTCTGTGCACTCCAGAAATATCTGACACAGAGGTGTTAAGAT 970
 DB 901 GCCACATGAAAGCATTTCTGTGCACTCCAGAAATATCTGACACAGAGGTGTTAAGAT 960
 QY 971 AATGACTATGGCCGAGACAGTGAAGCTGTGGGGCTTGAAGTATGATGAAATGATG 1030
 DB 961 AATGACTATGGCCGAGACAGTGAAGCTGTGGGGCTTGAAGTATGATGAAATGATG 1020
 QY 1031 TGTGGAGGTTACCTTTCTACAAACGAGACATGAGAAACCTTTTGAATTAATTAATG 1090
 DB 1021 TGTGGAGGTTACCTTTCTACAAACGAGACATGAGAAACCTTTTGAATTAATTAATG 1080
 QY 1091 GAAGACATTAATTTCTTGAAACCTCTCTTCAAGATGCAAAATCATTTGCTTTCAAGGCT 1150
 DB 1081 GAAGACATTAATTTCTTGAAACCTCTCTTCAAGATGCAAAATCATTTGCTTTCAAGGCT 1140
 QY 1151 TTGATTAAGATTCAAATTAAGCCCTTGGTGGAGGACAGATGATGCAAAAAGATTAATG 1210
 DB 1141 TTGATTAAGATTCAAATTAAGCCCTTGGTGGAGGACAGATGATGCAAAAAGATTAATG 1200
 QY 1211 AGACACAGTTTCTTCTCTGAGTAACTGGCAAGATGATATGATTAAGCTTGTACT 1270
 DB 1201 AGACACAGTTTCTTCTCTGAGTAACTGGCAAGATGATATGATTAAGCTTGTACT 1260
 QY 1271 CCTTTAAACCTGAAAGTAACTGTGACAGATCTAGATATTTTGTATGAAAGATTAAC 1330
 DB 1261 CCTTTAAACCTGAAAGTAACTGTGACAGATCTAGATATTTTGTATGAAAGATTAAC 1320
 QY 1331 GGTCAACATTAACATTAACACACCTGAAAATATGAGAGATGATGATGCTGCATG 1390
 DB 1321 GGTCAACATTAACATTAACACACCTGAAAATATGAGAGATGATGATGCTGCATG 1380
 QY 1391 GAACAATGAGAGCGGCGGCAATTTCTCAATTTTCTACTCTGCAAGTGAAGAGATTA 1450
 DB 1381 GAACAATGAGAGCGGCGGCAATTTCTCAATTTTCTACTCTGCAAGTGAAGAGATTA 1440

RESULT 8
 ABL50839
 ID ABL50839 standard; cDNA; 1440 BP.
 XX
 AC ABL50839;

XX	20-JUN-2002	(first entry)
DT		
DE	Human Akt3 encoding cDNA SEQ ID NO:10.	
XX		
KW	Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;	
KW	apoptosis; serine/threonine kinase; heat shock protein; anticancer;	
KW	cytostatic; cardiant; vasotropic; hepatotropic; neuroprotective;	
KW	antidiabetic; nootropic; cancer; diabetes; Alzheimer's disease;	
XX	cell death; radiation; brain ischaemia; cardiac ischaemia; gene; ss.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..1440
FT		/*tag= a
FT		/product= "Akt3"
XX		
PN	WO200215925-A1.	
PD	28-FEB-2002.	
PF	22-AUG-2001; 2001WO-JP0071179.	
XX		
PR	22-AUG-2000; 2000JP-00251529.	
XX		
PA	(KYOM) KYOMA HAKKO KOGYO KK.	
XX	(TSUR/) TSURUO T.	
PI	Tsuruo T, Fujita N, Sato S;	
XX		
DR	WPI; 2002-292035/33.	
XX	P-PSDB; ABB06998.	
PT	Regulation of apoptosis by promoting or inhibiting the intracellular	
PT	binding of Akt with Hsp90, useful for prevention and treatment of	
PT	apoptosis-regulation associated diseases including cancer.	
XX		
PS	Disclosure; Page 87-89; 93pp; Japanese.	
XX		
CC	The present invention describes the regulation of apoptosis, in which the	
CC	intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a	
CC	heat-shock protein) is promoted or inhibited. The present invention also	
CC	describes: (1) isoforms of Akt and Hsp90, and their partial peptides	
CC	including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA	
CC	encoding Akt or Hsp90 or their partial peptides including the binding	
CC	domain; (4) expression vectors containing the DNA; (5) host cells	
CC	transformed by the vectors; (6) production of Akt or Hsp90 or their	
CC	partial peptides including the binding domain by culture of the	
CC	transformed cells; (7) screening compounds for their ability to modify	
CC	intracellular Akt activity by contact with cells expressing Akt or Hsp90;	
CC	and (8) drug compositions containing antibodies recognizing the binding	
CC	domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and	
CC	Hsp90 have cytosstatic, cardiant, vasotropic, hepatotropic, antidiabetic,	
CC	neuroprotective and nootropic activities. Blockade of the binding of	
CC	Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.	
CC	Akt and Hsp90 can be used in the prevention and treatment of diseases	
CC	with which apoptosis regulation is associated, including cancer (such as	
CC	gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and	
CC	prostate cancer), diabetes, Alzheimer's disease, cell death caused by	
CC	radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The	
CC	present sequence encodes human Akt3 which is used in the exemplification	
CC	of the present invention	
XX		
SQ	Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;	
	Query Match	93.1%; Score 1440; DB 6; Length 1440;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1440; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	11 ATGACCGCATGTTCACATTGTGTGAAGAAGGTGGGTTCCAGAAAGGGGAGAAATATATATAAA 70	
DB	1 ATGACCGCATGTTCACATTGTGTGAAGAAGGTGGGTTCCAGAAAGGGGAGAAATATATATAAA 60	

QY	71	AACTGAGGCCAATAATCTTCCCTTTTGAAGAAGATGGCTCATTGATAGGATATAAAG	130
Db	61	AACGTGAGGCCAATAATCTTCCCTTTTGAAGAAGATGGCTCATTGATAGGATATAAAG	120
QY	131	AAACCTCAAGATGTGGAATTTACTTATCCCTCAACAATCTTTCAGTGGCAAAATGGCAG	190
Db	121	AAACCTCAAGATGTGGAATTTACTTATCCCTCAACAATCTTTCAGTGGCAAAATGGCAG	180
QY	191	TTTAATGAAAACAGAACGACCAAGCCAAACACATTTATCAGATGTCTTCAGTGGACT	250
Db	181	TTTAATGAAAACAGAACGACCAAGCCAAACACATTTATCAGATGTCTTCAGTGGACT	240
QY	251	ACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGGAAAAGGAAATGACAGAA	310
Db	241	ACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGGAAAAGGAAATGACAGAA	300
QY	311	GCTATCCAGGCTGTAGCAGACAGACTGCAAGGCAAGAGAGAGAGAAATGAAATTTAGT	370
Db	301	GCTATCCAGGCTGTAGCAGACAGACTGCAAGGCAAGAGAGAGAGAAATGAAATTTAGT	360
QY	371	CCAACCTCACAAATTTGAATATATGTAGAGAGGAAACAGATGGAATGCAATCCATCAT	430
Db	361	CCAACCTCACAAATTTGAATATATGTAGAGAGGAAACAGATGGAATGCAATCCATCAT	420
QY	431	AAAAGAAAAGCAATGAATGATTTTGACTATTTGAACTACTAGGTAAAGCATTTTGGG	490
Db	421	AAAAGAAAAGCAATGAATGATTTTGACTATTTGAACTACTAGGTAAAGCATTTTGGG	480
QY	491	AAAGTTATTTTGGTTCGAGAGAGAGGCAAGTGGAAAATCTATGCTATAGAAATCTGAG	550
Db	481	AAAGTTATTTTGGTTCGAGAGAGAGGCAAGTGGAAAATCTATGCTATAGAAATCTGAG	540
QY	551	AAAGAAAGCATTTATTCGAAAGAGTGAAGTGGCAACACTCTAACTGAAAGCAGAGTATTA	610
Db	541	AAAGAAAGCATTTATTCGAAAGAGTGAAGTGGCAACACTCTAACTGAAAGAGAGTATTA	600
QY	611	AAAGAACTAGACATCCCTTTTAAACATCCTTGAATATTTCTTCAGACAAAAGACCGT	670
Db	601	AAAGAACTAGACATCCCTTTTAAACATCCTTGAATATTTCTTCAGACAAAAGACCGT	660
QY	671	TTGTGTTTGTGATGGAATATGTTAATGGGGGGCAGCGTTTTTCCATTTTGCAGAGAG	730
Db	661	TTGTGTTTGTGATGGAATATGTTAATGGGGGGCAGCGTTTTTCCATTTTGCAGAGAG	720
QY	731	CGGGTGTCTCTGAGGACCGGCAACGTTTCTATGATGTCAGAAATTTGTCTGCTTGGAC	790
Db	721	CGGGTGTCTCTGAGGACCGGCAACGTTTCTATGATGTCAGAAATTTGTCTGCTTGGAC	780
QY	791	TATCTACATTTCCGAAAAGATTTGTGTACCGTGTATCTCAAGTTGGAGAACTTATGCTGGAC	850
Db	781	TATCTACATTTCCGAAAAGATTTGTGTACCGTGTATCTCAAGTTGGAGAACTTATGCTGGAC	840
QY	851	AAAGTGGCCACATTAATAATTAAGATTTTGGACTTTTGCAAAAGAAAGGATCACAGATGCA	910
Db	841	AAAGTGGCCACATTAATAATTAAGATTTTGGACTTTTGCAAAAGAAAGGATCACAGATGCA	900
QY	911	GCCAACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACAAGAGTGTGAAGAT	970
Db	901	GCCAACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACAAGAGTGTGAAGAT	960
QY	971	AATATCATATGGCCGAGACATGAGCTGGATGGGGGCTAGAGGGTGTCAATGTAAGAAATAGT	1030
Db	961	AATATCATATGGCCGAGACATGAGCTGGATGGGGGCTAGAGGGTGTCAATGTAAGAAATAGT	1020
QY	1031	TGTGGAGAGTTACCTTTCTACAAACAGAGCCATGAGAACTTTTGAATTAATTAATG	1090
Db	1021	TGTGGAGAGTTACCTTTCTACAAACAGAGCCATGAGAACTTTTGAATTAATTAATG	1080
QY	1091	GAAAGCATTAATTTCTCTCGAAGACTCTCTTCAAGATGCAAAATATATGCTTTCAGGGCTC	1150
Db	1081	GAAAGCATTAATTTCTCTCGAAGACTCTCTTCAAGATGCAAAATATATGCTTTCAGGGCTC	1140

QY 1151 TTGATTAAGAGATCCAAATAAACGCCCTGTGTGAGACACGATGATGCATAAAAGAAATTATG 1210
 |||||
 DB 1141 TTGATTAAGAGATCCAAATAAACGCCCTGTGTGAGACACGATGATGCATAAAAGAAATTATG 1200
 |||||
 QY 1211 AGACACAGTTCTTCTCTGTGAGTAAACCTGGCAAGATGATATATATAAAAGCTTGTACCT 1270
 |||||
 DB 1201 AGACACAGTTCTTCTCTGTGAGTAAACCTGGCAAGATGATATATATAAAAGCTTGTACCT 1260
 |||||
 QY 1271 CCTTTAAACCTCAAGTAACATCTGAGACGATACCTATATTTTGTATGAAGAAATTACA 1330
 |||||
 DB 1261 CCTTTAAACCTCAAGTAACATCTGAGACGATACCTATATTTTGTATGAAGAAATTACA 1320
 |||||
 QY 1331 GCTCAGACTATTACATTAACACCACTGAAATAATGATGAGATGGTATGACTGATG 1390
 |||||
 DB 1321 GCTCAGACTATTACATTAACACCACTGAAATAATGATGAGATGGTATGACTGATG 1380
 |||||
 QY 1391 GACCAATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGGACGAGATA 1450
 |||||
 DB 1381 GACCAATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGGACGAGATA 1440
 |||||

RESULT 9
 AAA96637
 ID AAA96637 standard; DNA; 1570 BP.
 XX
 AC AAA96637;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE DNA encoding a human Akt3 polypeptide.
 XX
 KM Human: Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;
 KM hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;
 KM reperfusion injury; myocardial ischemia reperfusion injury; stroke;
 KM liver damage; renal failure; organ transplantation; coronary artery; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..1523
 FT /*tag= a
 FT /product= "Akt3"
 XX
 PN MO200056866-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 14-MAR-2000; 2000MO-US006574.
 XX
 PR 19-MAR-1999; 99US-0125108P.
 XX
 PA (AVET) AVENTIS PHARM PROD INC.
 XX
 PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
 XX
 DR MPI: 2000-638260/61.
 DR P-PSDB; AAB19011.
 XX
 PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell
 PT death induced by apoptosis stimulating kinase 1 useful for treating
 PT myocardial infarction or ischemia reperfusion injury.
 XX
 PS Claim 3; Page 62-64; 73pp; English.
 XX
 CC The present sequence encodes a human Akt3 protein. Expression of Akt3
 CC prevents apoptotic cell death induced by apoptotic stimulating kinase 1
 CC (ASK1). The Akt3 polypeptide is useful for inhibiting cell death.
 CC preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or
 CC necrosis in a patient suffering from myocardial infarction or ischemia
 CC reperfusion injury. The polypeptide is also useful for treating
 CC myocardial infarction or ischemia reperfusion injury, where the
 CC reperfusion injury is myocardial ischemia reperfusion injury or is
 CC associated with stroke, liver damage, renal failure, organ

CC transplantation or coronary artery by pass grafting
 XX
 SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;
 Query Match 88.2%; Score 1364.8; DB 3; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 GGGAGTCATCATGAGGAGTTCACCTTTGTGAAGAAAGTGGGTCACAGAGGGGAGA 60
 |||||
 DB 116 GGGAGTCATCATGAGGAGTTCACCTTTGTGAAGAAAGTGGGTCACAGAGGGGAGA 175
 |||||
 QY 61 ATATATAAACTGGAGGCCAAGATACCTCTTTGAAGACAGATGGCTCATATAG 120
 |||||
 DB 176 ATATATAAACTGGAGGCCAAGATACCTCTTTGAAGACAGATGGCTCATATAG 235
 |||||
 QY 121 ATATAAAGAAACCTCAAGATGTGATTTACCTTATCCCTCAACAATTTTCACTGTC 180
 |||||
 DB 236 ATATAAAGAAACCTCAAGATGTGATTTACCTTATCCCTCAACAATTTTCACTGTC 295
 |||||
 QY 181 AAAATGCCAGTTATATGAAAAACAGACGACCAAAAGCCAAACATTTATATCAGATGCT 240
 |||||
 DB 296 AAAATGCCAGTTATATGAAAAACAGACGACCAAAAGCCAAACATTTATATCAGATGCT 355
 |||||
 QY 241 CCAGTGACACTAGTTATATGAGAAACATTCATATGATATCTCCAGAGAAAGGAGA 300
 |||||
 DB 356 CCAGTGACACTAGTTATATGAGAAACATTCATATGATATCTCCAGAGAAAGGAGA 415
 |||||
 QY 301 ATGACAGAAAGCTATCCAGGCTGTAGCAGACAGACTGACAGGCGAAGAGAGAGAAAT 360
 |||||
 DB 416 ATGACAGAAAGCTATCCAGGCTGTAGCAGACAGACTGACAGGCGAAGAGAGAGAAAT 475
 |||||
 QY 361 GAATTTAGTCCAACTTCAAAATGATATATGAGAGGAAAGATGATGCTCTAC 420
 |||||
 DB 476 GAATTTAGTCCAACTTCAAAATGATATATGAGAGGAAAGATGATGCTCTAC 535
 |||||
 QY 421 AACCCATCAATAAAGAAAGCAATGATTTTGAATTTGCTAATTAAGTAAAG 480
 |||||
 DB 536 AACCCATCAATAAAGAAAGCAATGATTTTGAATTTGCTAATTAAGTAAAG 595
 |||||
 QY 481 CACTTTGGGAAAGTTATTTTGGTTGAGAGAAAGGCAATGGAATACTATGCTATGAA 540
 |||||
 DB 596 CACTTTGGGAAAGTTATTTTGGTTGAGAGAAAGGCAATGGAATACTATGCTATGAA 655
 |||||
 QY 541 GATTCGAAAGAAAGATCATTTATGCAAGATGAAGTGCAACACCTCTAACTGAAG 600
 |||||
 DB 656 GATTCGAAAGAAAGATCATTTATGCAAGATGAAGTGCAACACCTCTAACTGAAG 715
 |||||
 QY 601 CAGAGATTAAAGAACACTAGACATCCCTTTTACATCTGGAATATCTCTCCAGAC 660
 |||||
 DB 716 CAGAGATTAAAGAACACTAGACATCCCTTTTACATCTGGAATATCTCTCCAGAC 775
 |||||
 QY 661 AAAAGACGTTTGTGTTTGTATGAGATATGTAATGAGGAGGAGCTGTTTCCATTT 720
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 DB 776 AAAAGACGTTTGTGTTTGTATGAGATATGTAATGAGGAGGAGCTGTTTCCATTT 835
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 QY 721 GTGAGAGAGCGGAGTCTTCTGAGAGCCGACACGTTTCTATGTGCGAAATGTCTC 780
 |||||
 DB 836 GTGAGAGAGCGGAGTCTTCTGAGAGCCGACACGTTTCTATGTGCGAAATGTCTC 895
 |||||
 QY 781 TGGCTTGACATCTACATTCGGAAGATGTGATCGGTATCTCAATGGAGATCT 840
 |||||
 DB 896 TGGCTTGACATCTACATTCGGAAGATGTGATCGGTATCTCAATGGAGATCT 955
 |||||
 QY 841 AATGCTGACAAAGATGCGCACATATAAATTAAGATTTTGAACCTTTGCAAAAGAGGAT 900
 |||||
 DB 956 AATGCTGACAAAGATGCGCACATATAAATTAAGATTTTGAACCTTTGCAAAAGAGGAT 1015
 |||||
 QY 901 CACAGATGACGCCACATGAAGACATTTCTGTGCACTCCAGAAATATCTGCAACAGAGT 960
 |||||
 DB 1016 CACAGATGACGCCACATGAAGACATTTCTGTGCACTCCAGAAATATCTGCAACAGAGT 1075
 |||||
 QY 961 GTTAGAAGATATATGACTATGCGGACATAGACTGTGTGGGCGCTATGAGGTTCTATGTA 1020
 |||||

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Db      1076 GTTAGAAGATATGACTATGAGCCAGACAGTGTGGGGCTGGGGTGTGATGTA 1135
Qy      1021 TGAATGATGTGGAGAGTTACCTTTTCACAAACGAGACATGAGAACTTTTGAAT 1080
Db      1136 TGAATGATGTGGAGAGTTACCTTTTCACAAACGAGACATGAGAACTTTTGAAT 1195
Qy      1081 AATATTATGAGAAACATTAATTTCTGGAACACTCTCTTCAGATGCAAAATCATTTGCT 1140
Db      1196 AATATTATGAGAAACATTAATTTCTGGAACACTCTCTTCAGATGCAAAATCATTTGCT 1255
Qy      1141 TTCAGGGCTCTTGATTAAGATCCAAATTAACGCTTGGTGAAGACAGATGATGCANA 1200
Db      1256 TTCAGGGCTCTTGATTAAGATCCAAATTAACGCTTGGTGAAGACAGATGATGCANA 1315
Qy      1201 AATAATTATGAGACACAGTTCTCTCTGAGATTAACCTGCAAGATGTATATGATTAANA 1260
Db      1316 AATAATTATGAGACACAGTTCTCTCTGAGATTAACCTGCAAGATGTATATGATTAANA 1375
Qy      1261 GCTTGACCTCTCTTTAAACCTCAAGTACATCTGAGACAGATTAATGATTTTGAATGA 1320
Db      1376 GCTTGACCTCTCTTTAAACCTCAAGTACATCTGAGACAGATTAATGATTTTGAATGA 1435
Qy      1321 AGAATTATCAGCTCAGACTATTAACATTAACACCACTGAAATATATGATGAGATGTAT 1380
Db      1436 AGAATTATCAGCTCAGACTATTAACATTAACACCACTGAAATATATGATGAGATGTAT 1495
Qy      1381 GGACTGCATGACAAATGAGA 1400
Db      1496 TGGCATGTCTGGGTAACTGGA 1515

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RESULT 10

AAH79025

ID AAH79025 standard, cDNA, 1570 BP.

XX AAH79025;

DT 31-JAN-2002 (first entry)

XX Human Akt3 encoding cDNA SEQ ID NO 1.

XX Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;
 KW cerebroprotective; neurotrophic; neuroprotective; antiarthritic;
 KW osteopathic; vasotropic; hepatotrophic; inhibitor of apoptosis; ASK1;
 KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;
 KW ischaemia reperfusion injury; stroke; organ transplantation;
 KW coronary artery bypass; tumour cell survival; gene therapy;
 KW Alzheimer's disease; osteoarthritis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 126..1523

FT /tag= a

PN /product= "Akt3"

XX MO200168850-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-US007663.

XX 14-MAR-2000; 2000US-00526043.

XX (AVERT) AVENTIS PHARM PROD INC.

XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;

XX MPI: 2001-582452/65.

XX P-PSDB; AAG78018.

XX New nucleic acid encoding human Akt3 protein, useful for inhibiting cell

PT death and treating myocardial infarction, ischemia reperfusion injury
 PT associated with stroke, liver damage and renal failure.

PS Claim 1, Page 59-62; 73pp; English.

XX The invention relates to human Akt3 protein (AH/PH-domain containing
 CC serine/threonine kinase, Akt) comprising a fully defined sequence
 CC (AA78018) of 465 amino acids, its splice variant or allelic variant,
 CC where the encoding polynucleotide hybridizes under stringent conditions
 CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570
 CC base pairs defined in the specification. Akt3 has cerebroprotective,
 CC neurotrophic, neuroprotective, antiarthritic, vasotropic and
 CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis
 CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a
 CC regulatory region is useful for inhibiting cell death in cardiac myocytes
 CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial
 CC infarction or ischaemia reperfusion injury, particularly that associated
 CC with stroke, liver damage, renal failure, organ transplantation or
 CC coronary artery bypass grafting. Agent of Akt3 are useful for improving
 CC Akt3 activity during treatment of patients suffering from myocardial
 CC infarction or ischaemia reperfusion injury and inhibitors of Akt3
 CC activity decrease tumour cell survival and result in tumour regression.
 CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the
 CC quantity of cell death and final infarct size, resulting in improved post
 CC -infarction function, improved quality of life and reduced mortality. In
 CC patients with existing heart failure, gene therapy with Akt3 retards the
 CC process of ventricular dilation and slows down disease progression. Akt3
 CC gene therapy is useful for treating other disease states, involving cell
 CC death by apoptosis, including Alzheimer's disease, liver degeneration or
 CC osteoarthritis

SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Query Match 88.2%; Score 1364.8; DB 4; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

Qy      1 GGGAGTCATCATGACGATGTTACCATGTTGAAAGAGTTGGTTCAAGAGGGGAGA 60
Db      116 GGGAGTCATCATGACGATGTTACCATGTTGAAAGAGTTGGTTCAAGAGGGGAGA 175
Qy      61 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 120
Db      176 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 235
Qy      121 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 180
Db      236 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 295
Qy      181 AAAATGCCAGTTATATATATATATATATATATATATATATATATATATATATATATAT 240
Db      296 AAAATGCCAGTTATATATATATATATATATATATATATATATATATATATATATATAT 355
Qy      241 CCAATGACACTCTGTTATATATATATATATATATATATATATATATATATATATATATAT 300
Db      356 CCAATGACACTCTGTTATATATATATATATATATATATATATATATATATATATATATAT 415
Qy      301 ATGACAGAAAGCTATATATATATATATATATATATATATATATATATATATATATATAT 360
Db      416 ATGACAGAAAGCTATATATATATATATATATATATATATATATATATATATATATATAT 475
Qy      361 GAATGTATGTCCTCACTTCAAAATGATATATATATATATATATATATATATATATATATAT 420
Db      476 GAATGTATGTCCTCACTTCAAAATGATATATATATATATATATATATATATATATATATAT 535
Qy      421 AACCATCATATATATATATATATATATATATATATATATATATATATATATATATATAT 480
Db      536 AACCATCATATATATATATATATATATATATATATATATATATATATATATATATATAT 595
Qy      481 CACTTTGGGAAAGTTATATATATATATATATATATATATATATATATATATATATATATAT 540
Db      596 CACTTTGGGAAAGTTATATATATATATATATATATATATATATATATATATATATATATAT 655

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QY 541 GATTCTGAAGAAAGATCATTAATTCGAAGAGTGAAGTGGACACACTCTAACTGAAG 600
  |||
Db 656 GATTCTGAAGAAAGATCATTAATTCGAAGAGTGAAGTGGACACACTCTAACTGAAG 715
QY 601 CAGAGTATTAAAGAACCTAGACATCCCTTTTAACTCCTTGAATATTCCTTCCAGAC 660
  |||
Db 716 CAGAGTATTAAAGAACCTAGACATCCCTTTTAACTCCTTGAATATTCCTTCCAGAC 775
QY 661 AAAAGACCGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
  |||
Db 776 AAAAGACCGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 835
QY 721 GTCGAGAGAGCGGGGTGTCTCTGAGGACCGCACACGTTTCTATGTGTCAGAAATGTCTC 780
  |||
Db 836 GTCGAGAGAGCGGGGTGTCTCTGAGGACCGCACACGTTTCTATGTGTCAGAAATGTCTC 895
QY 781 TGCCTTGAATCTATCTAATCCGGAAGATTTGTGTACCGTGTCTCAAGTTGGAGATCT 840
  |||
Db 896 TGCCTTGAATCTAATCCGGAAGATTTGTGTACCGTGTCTCAAGTTGGAGATCT 955
QY 841 AATGCTGAGCAAGATGGCCACATTAATAATTAAGATTTTGACCTTGCAAGAGGAGAT 900
  |||
Db 956 AATGCTGAGCAAGATGGCCACATTAATAATTAAGATTTTGACCTTGCAAGAGGAGAT 1015
QY 901 CACAGATGACGACCATGAGACATTCGTGTGCACTCCGAAATATCTGSCACAGAGGT 960
  |||
Db 1016 CACAGATGACGACCATGAGACATTCGTGTGCACTCCGAAATATCTGSCACAGAGGT 1075
QY 961 GTTAGAAGATATGACTATGCGCGAGCAGTAGACTGTGGGGGCTTGAAGGTTTCAATGA 1020
  |||
Db 1076 GTTAGAAGATATGACTATGCGCGAGCAGTAGACTGTGGGGGCTTGAAGGTTTCAATGA 1135
QY 1021 TGAATATGATGTGGGAGGTACCTTTCTTCAACACAGACCATAGAAATTTTGAAT 1080
  |||
Db 1136 TGAATATGATGTGGGAGGTACCTTTCTTCAACACAGACCATAGAAATTTTGAAT 1195
QY 1081 AATATTAATGAAGACATTAATTTCTCTGCAACACTCTTCAAGTGCATTAATCATTTGCT 1140
  |||
Db 1196 AATATTAATGAAGACATTAATTTCTCTGCAACACTCTTCAAGTGCATTAATCATTTGCT 1255
QY 1141 TTCAGGCTCTTGAATGAAGATCCAAATAAACGCTTGTGTGAGACACAGATGATGAA 1200
  |||
Db 1256 TTCAGGCTCTTGAATGAAGATCCAAATAAACGCTTGTGTGAGACACAGATGATGAA 1315
QY 1201 AGAATATTATGACACAGTTTCTTCTGAGATTAATGCGCAAGATATATATATATAT 1260
  |||
Db 1316 AGAATATTATGACACAGTTTCTTCTGAGATTAATGCGCAAGATATATATATATAT 1375
QY 1261 GCTTGTACCTCTTTTAACTCAAGTAACTGAGACAGATTAATATTTTGAATGA 1320
  |||
Db 1376 GCTTGTACCTCTTTTAACTCAAGTAACTGAGACAGATTAATATTTTGAATGA 1435
QY 1321 AGAATTTACAGCTCAGACTATTAACAATTAACACCACTGAAAAATATGATGAGATG 1380
  |||
Db 1436 AGAATTTACAGCTCAGACTATTAACAATTAACACCACTGAAAAATATGATGAGATG 1495
QY 1381 GGAATGCAATGACAAATGAGA 1400
  |||
Db 1496 TGGCATGTGGGTAACTGGA 1515
  |||

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RESULT 11

AAA89264 standard; cDNA; 1570 BP.

AAA89264;

28-MAR-2001 (first entry)

Human serine/threonine protein kinase Akt3 cDNA.

Akt3; human; protein kinase; vascular endothelial growth factor; VEGF; inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; gene therapy;

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KM 58.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 126..1523
XX FT /*tag= a
XX
XX MO200077190-A2.
XX
XX PD 21-DEC-2000.
XX
XX PF 01-JUN-2000; 2000MO-US015098.
XX
XX PR 11-JUN-1999; 99US-0138724P.
XX
XX PR 03-NOV-1999; 99GB-00026058.
XX
XX PA (AVET ) AVENTIS PHARM PROD INC.
XX
XX PI Guo K, Ivashchenko Y, Clark K,
XX
XX DR WPI; 2001-025336/03.
XX
XX DR P-PSDB; AAB19996.
XX
XX PS
XX PT Inducing expression of vascular endothelial growth factor. useful for
XX treating an ischemic condition, e.g. cerebrovascular ischemia, renal
XX PT ischemia or pulmonary ischemia, comprises administering a
XX PT serine/threonine protein kinase Akt protein.
XX
XX Example 1; Page 55-58; 67pp; English.
XX
XX CC The present sequence is that of cDNA coding for human Akt3 (see
XX CC AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase
XX CC capable of inducing vascular endothelial growth factor (VEGF) expression.
XX CC The sequence was deduced from 2 cDNA clones isolated from a human heart
XX CC cDNA library using a human Akt3 partial clone as probe. Akt3 is shorter
XX CC than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no
XX CC significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of
XX CC the molecules. A claimed method of inducing expression of VEGF in a cell
XX CC involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding
XX CC such a protein. The cell is preferably from a patient suffering from an
XX CC ischemic condition, especially cerebrovascular, renal, pulmonary, limb
XX CC or myocardial ischaemia, or ischaemic, idiopathic or hypertrophic
XX CC cardiomyopathy. The result is beneficial collateral blood vessel
XX CC formation. A claimed method of inhibiting angiogenesis in a patient
XX CC suffering from a tumour, comprises inhibiting the level of Akt activity
XX CC in the patient, thereby inhibiting production of VEGF. The method
XX CC comprises introducing an Akt antisense nucleic acid, an intracellular
XX CC binding protein (e.g. a scFv) that specifically binds the Akt protein, or
XX CC a nucleic acid encoding a dominant negative form of an Akt
XX
XX SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

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Query Match 88.2%; Score 1364.8; DB 4; Length 1570;

Best local Similarity 98.4%; Pred. No. 0;

Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

QY 1 GGGAGTCATCATGAGGATGTTACCATTTGTGAAGAAGGTTGGTTCAGAAGAGGGAGA 60
  |||
Db 116 GGGAGTCATCATGAGGATGTTACCATTTGTGAAGAAGGTTGGTTCAGAAGAGGGAGA 175
QY 61 ATRTATTAATAAACTGGAGGCCCAAGATACCTCTTTTGAAGACAGATGCTCATTAAG 120
  |||
Db 176 ATRTATTAATAAACTGGAGGCCCAAGATACCTCTTTTGAAGACAGATGCTCATTAAG 235
QY 121 ATRTAAAGAGAACTCAAGATGTGATTACCTTATCCCTCAACAACTTTTCAGTGC 180
  |||
Db 236 ATRTAAAGAGAACTCAAGATGTGATTACCTTATCCCTCAACAACTTTTCAGTGC 295
QY 181 AAAATGCCAGTTAATGAAAAAGAAAGCAAGCAAGCAACATTTATATATCATGATGCT 240
  |||
Db 296 AAAATGCCAGTTAATGAAAAAGAAAGCAAGCAAGCAACATTTATATATCATGATGCT 355

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QY 241 CCAAGTGAAGTCTGTTATAGAGAAATTCTGATGATCTCCAGAGAAAGGAGAGA 300
 DB 356 CCAAGTGAAGTCTGTTATAGAGAAATTCTGATGATCTCCAGAGAAAGGAGAGA 415
 QY 301 ATGAGACAGAGCTATCCAGGCTGTACAGACAGATGCGAGGCAAGAGAGAGAAAT 360
 DB 416 ATGAGACAGAGCTATCCAGGCTGTACAGACAGATGCGAGGCAAGAGAGAGAAAT 475
 QY 361 GAATTTAGTCCAACTTCAAAATTGATATATAGAGAGAGAGAGATGGATGCTCTAC 420
 DB 476 GAATTTAGTCCAACTTCAAAATTGATATATAGAGAGAGAGATGGATGCTCTAC 535
 QY 421 AACCCATCAATAAAGAGAGCAATGATGATTTGATCTATTGAACTACTAGTAAAG 480
 DB 536 AACCCATCAATAAAGAGAGCAATGATGATTTGATCTATTGAACTACTAGTAAAG 595
 QY 481 CACTTTGGGAAAGTATTTTGGTGTGAGAGAGGCAAGTGGAAATCTATGCTATGAA 540
 DB 596 CACTTTGGGAAAGTATTTTGGTGTGAGAGAGGCAAGTGGAAATCTATGCTATGAA 655
 QY 541 GAATTTGAAGAAAGAGTCAATTTGCAAGAGTGAAGTGGCAACACTCTAACTGAAG 600
 DB 656 GAATTTGAAGAAAGAGTCAATTTGCAAGAGTGAAGTGGCAACACTCTAACTGAAG 715
 QY 601 CAGAGTATTAAAGACACTAGACATCCCTTTTAACTCTGAAATATCTCTCCAGAC 660
 DB 716 CAGAGTATTAAAGACACTAGACATCCCTTTTAACTCTGAAATATCTCTCCAGAC 775
 QY 661 AAAAGACCGTTGTGTTTGTGATGGAATATGTTATGGGGGAGACTGTTTTCATTT 720
 DB 776 AAAAGACCGTTGTGTTTGTGATGGAATATGTTATGGGGGAGACTGTTTTCATTT 835
 QY 721 GTGAGAGAGCGGCTGTTCTCTGAGAGCGCACACCTTTCTATGTCAGAAATTTCTC 780
 DB 836 GTGAGAGAGCGGCTGTTCTCTGAGAGCGCACACCTTTCTATGTCAGAAATTTCTC 895
 QY 781 TGCCTTGAATCTATCTAATCCGGAAGATGTGTAACGCTGATCTCAAGTTGAGAAAT 840
 DB 896 TGCCTTGAATCTATCTAATCCGGAAGATGTGTAACGCTGATCTCAAGTTGAGAAAT 955
 QY 841 AATGCTGACAAAGATGCGCACTAATAATACAGTTTGGACTTTGCAAGAGAGAT 900
 DB 956 AATGCTGACAAAGATGCGCACTAATAATACAGTTTGGACTTTGCAAGAGAGAT 1015
 QY 901 CACAGATGAGCCACCATGAAACATTTCTGTGCACTCCAGAAATCTGTGACACAGGT 960
 DB 1016 CACAGATGAGCCACCATGAAACATTTCTGTGCACTCCAGAAATCTGTGACACAGGT 1075
 QY 961 GTTAGAAGATATGACTATGCGGAGCAGTAGACTGTGCGGCTTAGGGGTTGTCTAT 1020
 DB 1076 GTTAGAAGATATGACTATGCGGAGCAGTAGACTGTGCGGCTTAGGGGTTGTCTAT 1135
 QY 1021 TGAAATGATGTGGAGAGTACCTTTCTAACAACAGACATGAGAAATCTTTGAAAT 1080
 DB 1136 TGAAATGATGTGGAGAGTACCTTTCTAACAACAGACATGAGAAATCTTTGAAAT 1195
 QY 1081 AATATTATGAGAAACATTAATTTCTGTGAACACTCTCTTCAGATGCAAAATCATTTGCT 1140
 DB 1196 AATATTATGAGAAACATTAATTTCTGTGAACACTCTCTTCAGATGCAAAATCATTTGCT 1255
 QY 1141 TTCAGGCTCTTGATTAAGGATCAAAATAAAGCCTTGTGTGAGAGACAGATGATCAAA 1200
 DB 1256 TTCAGGCTCTTGATTAAGGATCAAAATAAAGCCTTGTGTGAGAGACAGATGATCAAA 1315
 QY 1201 AGAAATTAAGAGACAGTTTCTCTGTGAGTAACTGCAAGATGTATATGATATAAA 1260
 DB 1316 AGAAATTAAGAGACAGTTTCTCTGTGAGTAACTGCAAGATGTATATGATATAAA 1375
 QY 1261 GCTTGTACTCTCTTTAAACCTCAAGTAACTGTGAGACAGATCTAGATATTTTGTATGA 1320
 DB 1376 GCTTGTACTCTCTTTAAACCTCAAGTAACTGTGAGACAGATCTAGATATTTTGTATGA 1435
 QY 1321 AGAATTTAAGCTCAGACTATTAACAATAACCACTGAAATAATGATGAGAGTGTAT 1380

DB 1436 AGAATTTACAGCTCAGACTATTAACAATAACCACTGAAATAATGATCAGACTCAGATTG 1495
 QY 1381 GGACTGCATGACATATGAGA 1400
 DB 1496 TGGCATGCTGGGTAACTGGA 1515
 RESULT 12
 ADG85244
 ID ADG85244 standard; DNA; 1570 BP.
 XX
 AC ADG85244;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human Chrysoosporium associated DNA.
 XX
 KW de; gene; beta-glucosidic bond; beta-xylosidic bond; human.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 126..1523
 FT /*tag=a
 XX /product= "Chrysoosporium associated protein"
 PN US2004002136-A1.
 XX
 PD 01-JAN-2004.
 XX
 PF 21-MAR-2003; 2003US-00394568.
 XX
 PR 06-OCT-1998; 98WO-BP006496.
 PR 06-OCT-1999; 99WO-NL000618.
 PR 13-APR-2000; 2000US-00548938.
 XX
 PA (EMBL/) EMBL/AB M. A.
 PA (BURL/) BURLINGAME R. P.
 PA (OLSO/) OLSON P. T.
 PA (SINI/) SINITSYN A. P.
 PA (PARR/) PARRICHE M.
 PA (BOUS/) BOUSSON J. C.
 PA (PYNN/) PYNNONEN C. M.
 PA (PUNT/) PUNT P. J.
 PA (VZEL/) VAN ZEIJL C. M. J.
 XX
 PI Email:arb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;
 PI Bousson JC, Pynnoneen CM, Punt PJ, Van Zeijl CMJ;
 XX
 DR WPI; 2004-061663/06.
 DR P-PsDB; ADG85245.
 XX
 PT Novel mutant Chrysoosporium strain comprising nucleic acid sequence
 PT encoding polypeptide of interest such as proteases and lipases, the
 PT nucleic acid sequence being operably linked to expression-regulating
 PT region.
 XX
 PS Disclosure; SEQ ID NO 1; 70pp; English.
 XX
 CC The invention relates to a mutant Chrysoosporium strain comprising a
 CC nucleic acid sequence encoding a polypeptide of interest. A mutant
 CC Chrysoosporium strain is useful for producing a polypeptide of interest by
 CC culturing a mutant Chrysoosporium strain under conditions permitting
 CC expression of the protein or polypeptide, and recovering the subsequently
 CC produced polypeptide of interest. The conditions further permit secretion
 CC of the protein or polypeptide of interest. The polypeptides are useful
 CC for hydrolysing beta-glucosidic bonds. A polypeptide is useful for
 CC hydrolysing beta-xylosidic bonds. The present sequence represents human
 CC Chrysoosporium associated DNA.
 XX
 SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

XX The present invention describes a composition (C1) which comprises a
 CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
 CC Also described: (1) identification of a mitogen-activated protein (MAP)
 CC kinase pathway inhibitor involving incubating an antiandrogen or a
 CC library of molecules with a cell containing an activatable MAP kinase
 CC pathway and selecting the molecules which inhibit the activation of the
 CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
 CC involving incubating a cell with hydroxyflutamide and potential
 CC inhibitor, and assaying the level of activation of MAP kinase pathway or
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
 CC cytosolic activity, and can be used as a MAP kinase inhibitor,
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
 CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
 CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
 CC prostate cancer inhibitor; and for reducing the number of prostate cancer
 CC cells in a sample. The composition C1 provides effective combination
 CC therapy as compared to prior therapies. The present sequence encodes
 CC chicken serine/threonine protein kinase (Akt1), which is used in the
 CC exemplification of the present invention.

XX Sequence 2277 BP; 672 A; 490 C; 549 G; 566 T; 0 U; 0 Other;

Query Match 55.0%; Score 850.6; DB 12; Length 2277;
 Best Local Similarity 76.0%; Pred. No. 3.4e-220;
 Matches 1106; Conservative 0; Mismatches 334; Indels 15; Gaps 4;

QY 5 GTCATCATGAGCAGTGTACCATTTGGAAGAGGTTGGTTAGAGAGGGAAGATAT 64
 DB 460 GCCATTATGATGATGAATAGATGATGAGAGAGATGCTCCAAAGAGAGAGATAT 519
 QY 65 ATAAAAATGAGAGGCGCAAGATCTCTTTTGAAGACAGATGGCTCATTCATAGATAT 124
 DB 520 ATCAAAACATGAGAGCGCCAGCGTATTTCTTTTAAAGATAGATGACATTCATGGCTAC 579
 QY 125 AAAAGAAACCTCAAGATGTGATTTAC--CTTATCCCTCAACAACCTTTTCAGTGGCA 181
 DB 580 AAGGAACGACCGCAACGCTTGACCAACGAGATCACTTTAATATCTTCAGATGACT 639
 QY 182 AATGCGACGTTATGAAAAAGAGAGAGCAAGCAAGCAACATTTTATTCAGATGCTTC 241
 DB 640 CAGTCGACGCTGATGAG 699
 QY 242 CAGTGACCTACTGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
 DB 700 CAGTGACCTACTGTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
 QY 302 TGGACAGAAAGCTATCCAGGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 361
 DB 760 TGGACAGAAAGCTATCCAACTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 819
 QY 362 AATTGATGCTCACTTCACAAATTTGATATATGAGAGAGAGAGAGAGATGCTTAC 421
 DB 820 GATTTAGATCTGCTCTCTAGATGATTAATTCAGGCTGAGAGAGATGCTTAC 879
 QY 422 ACCCATCATTA--AGAAAGACATGATGATTTGATTAATTTGATTAATTTGATTAAT 478
 DB 880 ACAG 939
 QY 479 GGCATTTTGGAGAGATTTTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 538
 DB 940 GGCATTTTGGAGAGATTTTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 999
 QY 539 AAGATTTCTAGAT 598
 DB 1000 AAAATTTCTAGAT 1059
 QY 599 AGCAGAGATTAAGAT 658
 DB 1060 AACCGTCTTTACAGAT 1119
 QY 659 ACAAGAT 718

DB 1120 ACACAGATCGCTTGTTGTTGTTATGAGATGCTAAAGAGAGAGATGTTTTCAT 1179
 QY 719 TTGTGATGTC 778
 DB 1180 CTGTGATGTT 1239
 QY 779 TCTGCTTGAGATCTATCTATTCATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 835
 DB 1240 TCAGGCGCTGATTAATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAG 1299
 QY 836 AATCTAATGCTGAT 895
 DB 1300 AATCTAATGCTGAT 1359
 QY 896 GGGATCAGAGATGAT 955
 DB 1360 GGCATTAAGATTTG 1419
 QY 956 GAGGTGTTAGAGATGAT 1015
 DB 1420 GAGGTGCTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1479
 QY 1016 ATGTATGAAGATGAT 1075
 DB 1480 ATGTATGAAGATGAT 1539
 QY 1076 GAATTAATTAATGAT 1135
 DB 1540 GAATTAATTAATGAT 1599
 QY 1136 TTGCTTTCAGAT 1195
 DB 1600 CTCTTGAT 1659
 QY 1196 GCAAGAT 1255
 DB 1660 GCAAGAT 1719
 QY 1256 AAAAAAGCTGATCTCTCTTTTAACTCAAGTGAATGAGAGAGAGATGATTTT 1315
 DB 1720 AAAAAAGCTGATCTCTCTTTTAACTCAAGTGAATGAGAGAGAGATGATTTT 1779
 QY 1316 GATGAAGATTTTACAGCTCAGATTTTCAATTAACATTAACATTAACATTAACAT 1375
 DB 1780 GATGAAGATTTTACAGCTCAGATTTTCAATTAACATTAACATTAACATTAACAT 1833
 QY 1376 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1435
 DB 1834 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1893
 QY 1436 AGTGAAGAGATTA 1450
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RESULT 14
 AAA09078
 ID AAA09078 standard; DNA; 2626 BP.
 AC AAA09078;
 AC
 AC
 DT 10-AUG-2000 (first entry)
 XX
 XX
 DE Wild type murine Akt coding sequence.
 XX
 XX Akt; protein kinase B; serine-threonine kinase; proto-oncogene; cardiant;
 KW inhibitor; apoptosis; cell death; antiapoptotic; muscular active; ss.
 OS Mus musculus.
 XX
 XX
 XX Key Location/Qualifiers
 FH 284..1726
 FT CDS
 FT /*tag= a

FT /product= "protein_kinase_B"
 XX
 PN WO200020025-A2.
 XX
 PD 13-APR-2000.
 XX
 PF 29-SEP-1999; 99WO-US022633.
 XX
 PR 02-OCT-1998; 98US-0102740P.
 XX
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
 XX
 PI Walsh K;
 XX
 DR WPI, 2000-303639/26.
 DR P-PDB; AAY92223.
 XX
 PT Treating myocardial infarction or conditions associated with increased
 PT apoptotic cell-death of vascular endothelial cells or skeletal myocytes
 PT comprises administering Akt (also termed Protein Kinase B (PKB))
 PT molecule.
 XX
 PS Disclosure; Page 69; 71pp; English.
 XX
 CC The invention concerns methods of treating myocardial infarction, which
 CC comprise administering to a subject an Akt (Protein Kinase B) molecule to
 CC inhibit cardiac tissue necrosis. Akt is a proto-oncogene which encodes a
 CC serine threonine kinase. It inhibits apoptotic cell death, in particular
 CC of cardiomyocytes, skeletal myocytes and/or vascular endothelial cells.
 CC It is therefore also useful for treating muscular dystrophy, spinal
 CC muscular atrophy, anabolic steroid-induced muscle injury, skeletal muscle
 CC oxidative stress, physical exercise and unloading-induced skeletal muscle
 CC atrophy. The Akt protein can also be used in screening for an inhibitory
 CC agent that inhibits apoptotic cell-death of cells
 XX
 SQ Sequence 2626 BP; 584 A; 767 C; 754 G; 521 T; 0 U; 0 Other;
 Query Match 48.6%; Score 751.4; DB 3; Length 2626;
 Best Local Similarity 71.8%; Pred. No. 3.2e-193;
 Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;
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 QY 68 AAAAATGAGGCGCAAGATACCTTCCTTTGAAGACAGATGCTCATTCATGATATATA 127
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 QY 128 GAGAAACCTCAAGATGTGAT---TTACCTTATCCCTCAACAACTTTCAATGAGCAAA 184
 DB 401 GAACGGCTTCAGATGTGATCAAGCGAGTCCCACTCAACAACTTCTAGTGGCAAA 460
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 DB 461 TGCAGTTAATGAAGACAGAACGACCAAGGCCCAACCTTTATCATCCCTGCTGACAG 520
 QY 245 TGGACCTATCTGTTATAGAGAACTTTTCATGTAGATCTCAAGAGAAAGGAAAGATGG 304
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 QY 365 TGTAGTCAACTTCACAATATGATATATAGAGAGAGAGATGATGCTCTACAAACC 424
 DB 641 TTCCGATCAGGCTCAACCACTGACACTCAAGGCGCTAAGAGATGAGGTCTCCCTGGCC 700
 QY 425 CATC---ATAAAAGAAAGACATGATGATTTGACTATTTGAACTTACCTAGTAAAGGC 481
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 DB 881 CGTGTCTCGAAGACTCTAGGCACTCCCTTCTTACCGGCCCTCAAGTACTCATTCAGACC 940
 QY 662 AAGACCGTTTGTGTTTGTGATGGAATATGTTAATGAGGGGAGAGCTTTTCCATTGG 721
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 QY 722 TCGAGAGAGGAGGTGTTCTCTGAGACCCACACAGTTTCTATGAGTCAAGAAATGTCT 781
 DB 1001 TCTGAGAGGCGCTGTCTCCAGAGACCGGGCCGCTTCTATGTGCGAGATTTGTCT 1060
 QY 782 GCTTGAGACTATCTACATTCGGAAAGA---TTGTGTACCGTGTCTCAAATTGAGAT 838
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 QY 1079 TTAATATTAATGAGACATTAATTTCTGCAACACTCTCTTCAATGCAAAATCATTTG 1138
 DB 1361 CTGATCTCATGAGAGAGATCCGCTTCCGCGCACTCGGCTTGAAGCAAGTCCCTG 1420
 QY 1139 CTTTCAGGCTCTTGATTAAGAGATCCAAATAAAGCTTGTGTGAGAGCAAGATGCA 1198
 DB 1421 CTCTCGGCGTGTCAAGAAAGACCTTACACAGAGGCTCGGTGGGCTCTGAGAGTGC 1480
 QY 1199 AAGAAATTAATGAGACAGATTTCTCTGAGATTAACCTGGAAGATGATATGATTA 1258
 DB 1481 AAGAGATCAATGAGACAGCGGTTCTTTCACATGCTGTGTGAGAGATGATATGAGAG 1540
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 QY 1319 GAAGAATTAACAGCTCAGATTAATTAATTAACCACTGAAAAAATATGATGAGATG 1378
 DB 1601 GAGAGATTAACAGCTCAGATGATCAACATCAACGCCCTG-----ATCAAGATGACAG 1654
 QY 1379 ATGAGCTGATGAGACATGAGAGCGCGGCAATTTCCCTCAATTTCTTACTGTGAAG 1438
 DB 1655 ATGAGATGTGTGACAGTGAAGCGAGAGCGCACTTCCCAAGTTCTTACTGACGCA 1714
 QY 1439 GAGAGAAATTAAGTC 1453
 DB 1715 GGCACAGCTGAGGC 1729
 RESULT 15
 AAD28550
 ID AAD28550 standard; cdNA; 2626 BP.
 XX

AC AAD28550;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Mouse Akt cDNA.
 XX
 KW Mouse; 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitor;
 KM HMG-CoA; angiogenesis; Akt protein; serine-threonine kinase; PKB;
 KM protein kinase B; vascular insufficiency; nonhypercholesterolaemic;
 KM nonhyperlipidaemic; hypertension; vascular disease; gangrene; wound;
 KM Buerger's syndrome; myocardial infarction; coronary artery disease;
 KM ischaemia; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 284..1726
 FT /tag= a
 FT /product= "Mouse Akt protein"
 XX
 PN MO200193806-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 05-JUN-2001; 2001WO-US018175.
 XX
 PR 08-JUN-2000; 2000US-00590740.
 XX
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
 XX
 PI Walsh K;
 XX
 DR WPI: 2002-164293/21.
 PT P-PSDB; AAE17784.
 PT
 PT Use of 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitor in
 PT promoting angiogenesis in a tissue of a subject to treat conditions e.g.
 XX hypertension.
 XX
 PS Disclosure; Page 68-69; 70pp; English.
 XX
 CC The invention relates to 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)
 CC reductase inhibitors and their use in promoting angiogenesis and in
 CC activating Akt polypeptides in vascular endothelial cells. Akt is a proto
 CC -oncogene encoding a serine-threonine kinase (also known as protein
 CC kinase B, PKB). The invention also relates to methods and compositions
 CC for the treatment of conditions associated with vascular insufficiency.
 CC HMG-CoA reductase inhibitors are used for treating nonhyperlipidaemic and
 CC /or nonhypercholesterolaemic subjects who are in need of increased blood
 CC flow to a tissue or promoting angiogenesis, to treat conditions such as
 CC hypertension, diabetic peripheral vascular disease, gangrene, Buerger's
 CC syndrome, wound (e.g. surgical wound), ischaemia of the muscle, brain,
 CC kidney, lung, heart and limb, severe occlusive and/or obstructive
 CC vascular disease, peripheral vascular disease, myocardial ischaemia,
 CC myocardial infarction, coronary artery disease, cerebral vascular disease
 CC and visceral vascular disease. The present sequence is mouse Akt cDNA
 XX
 SO Sequence 2626 BP; 584 A; 767 C; 754 G; 521 T; 0 U; 0 Other;
 Query Match 48.6%; Score 751.4; DB 6; Length 2626;
 Best Local Similarity 71.8%; Pred. No. 3.2e-193;
 Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;
 QY 8 ATCAGAGGAGTTCATTCATGGAAGAAGTGGCTCAGAAAGGGGGAATATTA 67
 DB 281 ACCATGAAGAGTACCATTCGTAAGAGGGCTGCTCACAAGAGGGGAAATATAT 340
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 DB 341 AAAAATGAGAGGCAAGATACCTCTTCCTCAGAAAGATGGCACTTTATTTGGCTACAG 400
 QY 128 GAGAAATCTCAAGATGGAT--TTACCTTATCCCTCAACAACATTTTCAAGTGGCAAA 184

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 QY 602 AGAGTATTAAGAAACATAGACATCCCTTTTAACTCTTGAATATTCCTTCAGACA 661
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Job time : 829 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-869-079b-1

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Searched: 1202784 seqs, 818139359 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	751.4	48.6	2626	4 US-09-590-740-5	Sequence 5, Appl1
3	721.2	46.6	2184	4 US-09-417-197-138	Sequence 138, Appl1
4	719.2	46.5	2610	2 US-09-212-771-1	Sequence 1, Appl1
5	719.2	46.5	2610	3 US-09-091-058-1	Sequence 1, Appl1
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8	716.4	46.3	2181	4 US-09-417-197-70	Sequence 70, Appl1
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12	604.4	39.1	1254	4 US-09-590-740-3	Sequence 1, Appl1
13	403	26.1	403	3 US-09-474-922A-1	Sequence 1, Appl1
14	383.8	17.2	387	4 US-09-474-922A-2	Sequence 2, Appl1
15	266.4	17.2	2239	4 US-09-949-016-1676	Sequence 1676, Appl1
16	261.2	16.9	3255	4 US-09-016-434-1471	Sequence 1471, Appl1
17	261.2	16.9	6102	4 US-09-949-016-2007	Sequence 2007, Appl1
18	260.4	16.8	2370	3 US-09-031-295-1	Sequence 1, Appl1
19	260.2	16.8	265	4 US-09-513-999C-2948	Sequence 2948, Appl1
20	258.8	16.7	1338	4 US-10-067-977-1	Sequence 1, Appl1
21	257.6	16.7	2599	6 526464-1	Patent No. 526464
22	257.6	16.7	2599	6 526464-1	Patent No. 526464
23	257.2	16.6	2311	2 US-08-712-709-6	Sequence 6, Appl1
24	257.2	16.6	2311	3 US-09-111-444-6	Sequence 6, Appl1
25	257.2	16.6	2311	3 US-09-541-228-6	Sequence 6, Appl1
26	257.2	16.6	2311	4 US-09-016-434-772	Sequence 772, Appl1
27	255.8	16.5	2396	4 US-09-949-016-1735	Sequence 1735, Appl1

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39	218	14.1	2324	4 US-09-190-976B-6	Sequence 6, Appl1
40	214.6	13.9	2705	4 US-09-949-016-839	Sequence 839, Appl1
41	214.6	13.9	2715	4 US-09-949-016-1959	Sequence 1959, Appl1
42	213	13.8	2754	4 US-09-429-322-3	Sequence 3, Appl1
43	211.6	13.7	2946	4 US-09-949-016-1991	Sequence 1991, Appl1
44	211.6	13.7	4438	4 US-09-566-921-81	Sequence 81, Appl1
45	206.6	13.4	2262	4 US-09-949-016-5805	Sequence 5805, Appl1

ALIGNMENTS

RESULT 1					
US-09-851-670-1					
Sequence 1, Application US/09851670					
Patent No. 6809194					
GENERAL INFORMATION:					
APPLICANT: Reinhard, Christoph					
APPLICANT: Jefferson, Anne B.					
TITLE OF INVENTION: AK3 INHIBITORS					
FILE REFERENCE: PP-01699.002/200130.520					
CURRENT APPLICATION NUMBER: US/09/851,670					
CURRENT FILING DATE: 2001-05-08					
NUMBER OF SEQ ID NOS: 27					
SOFTWARE: FastSeq for Windows Version 4.0					
SEQ ID NO 1					
LENGTH: 1547					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-09-851-670-1					
Query Match					
Best Local Similarity 100.0%; Score 1547; DB 4; Length 1547;					
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	181	AAATATCCAGTTAATGAAGAAAGCAAGCAACCAATTTATATATGATGTCT	240		
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QY	301	ATGGAAGAGAGTATCCAGGCTGTAGACAGATGCGAGAGCAAGAGAGAGAT	360		
DB	301	ATGGAAGAGAGTATCCAGGCTGTAGACAGATGCGAGAGCAAGAGAGAGAT	360		
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QY 961 GTTAGAAGATTAATGATGATGCGAGAGATGATGATGATGATGATGATGATGAT 1020
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QY 1021 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AATATTAAATGAGAAATTAATTTCTGGAACAATCTCTGAGATGCAAAATCATGCT 1140
DB 1081 AATATTAAATGAGAAATTAATTTCTGGAACAATCTCTGAGATGCAAAATCATGCT 1140
QY 1141 TTCAGGGCTCTTGATTAAGGATCCAATTAACGCTTGTGAGAGACCAAGATGATCA 1200
DB 1141 TTCAGGGCTCTTGATTAAGGATCCAATTAACGCTTGTGAGAGACCAAGATGATCA 1200
QY 1201 AGAAATTAATGAGAAATTAATTTCTGGAACAATCTCTGAGATGCAAAATCATG 1260
DB 1201 AGAAATTAATGAGAAATTAATTTCTGGAACAATCTCTGAGATGCAAAATCATG 1260
QY 1261 GCTTGATCCTCTTTAAACCTCAAGTAACTGAGAGATGATGATGATGATGATGAT 1320
DB 1261 GCTTGATCCTCTTTAAACCTCAAGTAACTGAGAGATGATGATGATGATGATGAT 1320
QY 1321 AGAATTTAGAGCTCAGACTATTAACAATTAACCACTGAAATATGATGAGATGAT 1380
DB 1321 AGAATTTAGAGCTCAGACTATTAACAATTAACCACTGAAATATGATGAGATGAT 1380
QY 1381 GGAATTTAGAGCTCAGACTATTAACAATTAACCACTGAAATATGATGAGATGAT 1440
DB 1381 GGAATTTAGAGCTCAGACTATTAACAATTAACCACTGAAATATGATGAGATGAT 1440
QY 1441 ACGAGATTAAGTCTCTTCAATCTGCTACTCACTGCTCACTTCAATTTAATGAAAA 1500
DB 1441 ACGAGATTAAGTCTCTTCAATCTGCTACTCACTGCTCACTTCAATTTAATGAAAA 1500

QY 1501 TGATTCCTGAGCATCAGCATCTAGCTCTTACATAGAGGGGCA 1547
DB 1501 TGATTCCTGAGCATCAGCATCTAGCTCTTACATAGAGGGGCA 1547

RESULT 2
US-09-590-740-5
; Sequence 5, Application us/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-590-740-5

Query Match
Best Local Similarity 71.8%; Score 751.4; DB 4; Length 2626;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

QY 8 ATCATGAGGATGTTACATTTGTAAGAGGTTGGTTCAGAGAGGGAGATATATA 67
DB 281 ACCATGAACGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 340
QY 68 AAAAATGAGGCGCAAGATCTCTTTTGAAGACAGATGCTATGATGATGATGAT 127
DB 341 AAAAATGAGGCGCAAGATCTCTTTTGAAGACAGATGCTATGATGATGATGAT 400
QY 128 GAGAAATCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 184
DB 401 GAGAAATCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 460
QY 185 TGCCAGTTAATGAAGAAAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCA 244
DB 461 TGCCAGTTAATGAAGAAAGCAAGAGCAAGAGCAAGAGCAAGAGCAAGAGCA 520
QY 245 TGAGATCTGTTATGAGAGAACTTTTATGATGATGATGATGATGATGATGAT 304
DB 521 TGAGATCTGTTATGAGAGAACTTTTATGATGATGATGATGATGATGATGAT 580
QY 305 ACAGAACTATCAGGCTGTAGCAGACAGCTGAGAGCAAGAGCAAGAGCAAGAG 364
DB 581 ACAGAACTATCAGGCTGTAGCAGACAGCTGAGAGCAAGAGCAAGAGCAAGAG 640
QY 365 TGATGCTCAACTTCAAAATGATATATGAGAGAGAGAGAGAGAGAGAGAGAG 424
DB 641 TGATGCTCAACTTCAAAATGATATATGAGAGAGAGAGAGAGAGAGAGAGAG 700
QY 425 CATC---ATTAAGAAAGCAATGATGATGATGATGATGATGATGATGATGAT 481
DB 701 CATC---ATTAAGAAAGCAATGATGATGATGATGATGATGATGATGATGAT 760
QY 482 ACTTTTGGAAAGTATTTGGTTCGAGAGAGCAAGAGCAAGAGCAAGAGCAAGAG 541
DB 761 ACTTTTGGAAAGTATTTGGTTCGAGAGAGCAAGAGCAAGAGCAAGAGCAAGAG 820
QY 542 ATTCTGAAGAAAGAGTATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
DB 821 ATTCTGAAGAAAGAGTATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 880
QY 602 AAGATTTAAGAAACATGAGATGATGATGATGATGATGATGATGATGATGAT 661
DB 881 AAGATTTAAGAAACATGAGATGATGATGATGATGATGATGATGATGATGAT 940


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OY 662 AAAGCCGTTTGTTTGATGGAATATGTAAATGGGGGCGAGCTGTTTTCATTG 721
Db 941 CACGACCCCTCTGCTTGTGTCATGAGTATGCAACGGGGGCGAGCTTCTTCCACCTG 1000
OY 722 TCGAGAGCGGGGTGTTCTCTGAGGACCGCACACGTTTCTATATGATGCAAAATGTCTCT 781
Db 1001 TCTGAGAGCGGGGTGTTCTCTGAGGACCGGGGCGAGCTTCTATATGATGCGAATGTGTCT 1060
OY 782 GCCTTGAATATCTATCATTTCCGAAAGA--TTGTGTAACGTTGATCTCAAGTTGGAGAT 838
Db 1061 GCCCTGGACTCTTCTGACCTCCGAGAAACGTGTGTCACCGGACCTGAACCTGGAGAAC 1120
OY 839 CTAAATGCTGCAAAAGATGCGCACATAAAATACAGATTTTGGACTTTGCAAAAGAGG 898
Db 1121 CTCAATGCTGCAAAAGAGCGGACATCAAGATTAACGACTTCTGGGCTGTGCAAGAGAGGG 1180
OY 899 ATCAAGATGACGACCATGAAAGATTTCTGTGCACTCCAGAAATATCTGACCAAG 958
Db 1181 ATCAAGATGCTGCACTATGAGACATTTCTGCGAAGCGCGGAGTACTTGGCCCTGAG 1240
OY 959 GTGTTAGAAGATTAATGACTATAGCCGAGCAGTAGACTGTGGGGCTTATGGGTTGTCA 1018
Db 1241 GTGCTGAGAGCAACAGCACTACGGCCGTGCAATGAGCTGTGGGGGCTGGGGTGTATG 1300
OY 1019 TATGAATATGATGTGTGCGAGGTACTTCTTACCAACGAGCATGAGAACTTTTGA 1078
Db 1301 TATGAGATGATGTGTGCGCGCTGCTTCTTACCAACGAGCATGAGAACTGTTGAG 1360
OY 1079 TTAATATTAATGAGAAACATTAAATTTCTGGAACACTCTCTGATGCAAAATGATG 1138
Db 1361 CTGATCTCATATGAGAGATTCGCTTCCCGGACACATCGGCTTGAAGCCAAAGTCCCTG 1420
OY 1139 CTTTCAGGGCTCTTGTATAAAGATTCAAATTAACGCTTGTGTGAGAGCACGATGATGCA 1198
Db 1421 CTCTCGGGCTGTCTAAGAGGACCTTACACAGAGGCTCGGTGGGGGCTCTGAGGATGCC 1480
OY 1199 AAAGAAATTAATGAGACACAGTTTCTTCTGTGAGTAACTGGCAAGATGATATGATAA 1258
Db 1481 AAGGAGATCAATGACAGCACCGGTTCTTTCGCAACATCGTGTGAGAGATGTATAGAGAG 1540
OY 1259 AAGCTGTACCTCCTTTTAAACCTCAAGTAACTGACATCTGAGACAGATATATTTGAT 1318
Db 1541 AAGCTGAGCCCACTTTCAAGCCCAAGGTCACTCTGTGAGCTGACACCAAGTATTTGAT 1600
OY 1319 GAAGAAATTAAGACTCAGACTATTAACAATAACCACTGAAATAATATGATGAGATGCT 1378
Db 1601 GAGAGTTCAAGCTCAATATATCATCATCAACGCCGCTG-----ATCAAGATGACGAC 1654
OY 1379 ATGACATGACATGACATGAGAGCGCGCAGATTTCTCTCAATTTCTACTCTGCAAGT 1438
Db 1655 ATGAGATGTGTGAGACATGAGGAGCGGACCTTCCCGAGTTCTCTACTGAGCAGT 1714
OY 1439 GAGCAGAAATAGTC 1453
Db 1715 GGACACAGCTGAGGC 1729

RESULT 3
US-09-417-197-138
; Sequence 138, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole Thastrup, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417.197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA

```

	ORGANISM:	Artificial Sequence	
:	FEATURE:		
:	OTHER INFORMATION:	EGFP-PRE fusion	
:	FEATURE:		
:	NAME/KEY:	CDS	
:	LOCATION:	(1)..(2181)	
:	US-09-417-197-138		
	Query Match	46.6%; Score 721.2; DB 4; Length 2184;	
	Best Local Similarity	70.7%; Pred. No. 9,6e-207;	
	Matches 1021; Conservative	0; Mismatches 408; Indels 15; Gaps	4
OY	3	GAGTCATCATGACCGATTGTACCATTGGTGAAGAAGCTGGGCTTCAGAAAGGGGAGAAAT	62
Db	734	GAGGCACCAATGAGCCGACGGTGCTATTGTGAAGAGGGTTGGCTCACAAAAGAGGGGAGT	7933
OY	63	ATATAAAAACTGSGAGGCCAACAATCCTCTTTTGAACAGACGATGGGCTCATTAAGAT	1222
Db	794	AACITCAAAGACTTGGCGGCCACGCTACTTCTCTCAGAAATGATGGACCTTCAATTGGCT	8533
OY	123	ATAAAGGAAACCTCAAGATGTGATTTAACCTTA---TCCCCTGAACAACCTTTCACTGG	179
Db	854	ACAAGAGGGGGCCGACGATGTGGAACAACGTGAGGCTCCCTCAACAACCTTCTGTGG	9133
OY	180	CAAAATGCCAGTTATGAAAAAGAACGACCAAAAGCCAAACACTTATTAATCATGATGTC	239
Db	914	CGAGATGCCAGCTGATGAAAGCGAGCGGGCCCCGCCCAACACTTATCATCTCGCTGCC	9733
OY	240	TCCAGTGGACCTACTGTTATAGAGAAACAATTCAATGTATGATATCCAGAGAAAGGGAG	259
Db	974	TGAGTGGACCACTGTCAATGAAACGACACTTTCATGTGAGACTCTTGAGAGCGGGAGG	103
OY	300	AATGACAGAAAGCTATCCAGCGCTGTAGCAGACAGACTGCAGAGGCCAAGAAAGAGAGAA	359
Db	1034	AGTGGACAAACCGCATCCAGACCTGTGGCTGACCGGCTTAAGAACAGAGAGAGAGAGAG	109
OY	360	TGAATTGTAGTCCAATTCAAAATTGATTAATATAGAGAGAAAGATGATGCTCTTA	419
Db	1094	TGGACTTCGGGTGGGGCTCACCCAGATGCAACTCAGGGGGCTGAAGAGATGGAGGTGCC	115
OY	420	CAACCCATC---ATAAAGAAAGAAAGATGATTTTGAATATTGAATCTAGTGA	476
Db	1154	TGGCCAAAGCCCAAGCACCGCTGACCATGAACGATTGATGATCCTAAGCTGTGTGGCA	121
OY	477	AAGGCACTTTTGGGAAAGTTATTTTGGTTCAGAGAGAGGCAAGTGAAGAAATACTACTTA	536
Db	1214	AGGGCACTTTCCGAGAGATGATCTCTGTGAGAGAGAGAGCCACAGGCCGCTACTACGCCA	127
OY	537	TGAAGATTCTGAAGAAAGAGTCAATTATGTGAAGAGTAGAAGTGGCACACACTCTAACTG	556
Db	1274	TGAAGATCCTCAAGAAAGAAAGTCACTGTGGCAAGAGAGAGATGGGCCACACACTCACCG	133
OY	597	AAAGCAGAGTATTTAAAGAACTATGACTCCCTTTTAACTCTTGAATATTTCTTCC	656
Db	1334	AGAACCGCGTCTCGAGAACTCCAGAGCACCCCTTCTCACAGCCCTAAGTACTCTTCC	139
OY	657	AGACAAAGACCGTTTGGTTTTTGTGATGAAATATGTTAATGSGGGGGAGAGTGTTTTCC	716
Db	1394	AGACCAACAGACCGCTCTGTCTTGTCAATGAGATAGCCMAAGGGGGGAGAGTGTCTTCC	145
OY	717	ATTGTTCAGAGAGCGGGGTCTCTCTGAGGACCGCACAGTTTCTATGTGTCAGAAATTG	776
Db	1454	ACTGTCCGGGGAAAGGTGTGTCTTCGAGAGACCGGGCCCGTCTTATATGGGGCTGAAGTTG	151
OY	777	TCTCTGCTTTGACTATCTCACTTCCGAAAGA---TTGTGTACCGTGAATCTCAAGTTGG	833
Db	1514	TGTCAACCTCTGACTACCTGCACTCGAGAGAAAGAGTGTGTATCCGGGACCTCAAGCTGG	157
OY	834	AGAAATCTAATGCTGGGCAAAAGATGGCCATATAAATTTACAGATTTTGAAGTTTGGCAAG	893
Db	1574	AGAACTCATGTGAGCAAGAGCGGGCACATTAAGATCAAGACTTGGGGCTGTGCAAG	163
OY	894	AAAGGATCAAGATGAGCCACATGAAGACATTTCTGTGGCACTTCAGAAATATCTGGCAC	953

DB 1634 AGGGGATCAAGGCGGTGCGCACCATTGAAACCTTTTGCGGCAACCTGAGTACTTGCGCCC 1693
QY 954 CAGAGGTGTTAAGATTAATGACTATGACGCGAGCAGTATAGCTGGTGGGCTTAGGGGTTG 1013
DB 1694 CCGAGGTGCTGAGGACAAATGACTAGCGCGTGCAGTGAATGATGGGGGCTGGGGCTGG 1753
QY 1014 TCATGATGAAATGATGTGTGGAGGTACCTTTCTTCAACACGAGCAACATGAGAACTTT 1073
DB 1754 TCATGATGAGAGATGATGTGGGTGGCTGGCTGCTTCTTCAACACGAGCAACATGAGAACTTT 1813
QY 1074 TTGAATTAATTAATGAGAAACATTAAATTTCTTGAACACTCTTCTTCAATGCAAAAT 1133
DB 1814 TTGAGCTCATCTCAATGAGAGAGATCCGCTCCCGGCAAGCTTGGTCCCGAGGCCAAGT 1873
QY 1134 CATTCCTTCAAGGCTCTTGATTAAGATTCAAATTAAGCCCTTGGTGAAGACCGAGT 1193
DB 1874 CTTTGCTTTCAGGGCTGCTCAAGAGAGACCCCAAGCAAGAGCTTGGCGGGGCTCCGAGG 1933
QY 1194 ATGCAAAAGAAATTAATGAGACACAGTTTCTTCTGAGTAAACTGGCAAGATGATATG 1253
DB 1934 AGCCCAAGAGATCATGACAGCATCGCTTCTTGGCGTATCGTGTGGCAGACGTGTAG 1993
QY 1254 ATBAAAGCTTGTAACCTCTTTTAAACTCAAGTAAACATCTGAGACAGATPACTGATTT 1313
DB 1994 AGAAGAGCTCAGGCCACCTTCAGGCCCGAGGTCAAGTGGAGACTGACACAGGATTT 2053
QY 1314 TTGATGAGAAATTTAGAGCTCAGACTATTAACATTAACACCACTGAAATTAATGAGAG 1373
DB 2054 TTGATGAGAGTTTCAAGCGCCCAAGATATCAACATCAACCTGACCA-----GAGT 2107
QY 1374 ATGATGAGACTGTCATGACCAATGAGAGCGCGCATTTTCCCTCAATTTTCTACTCTG 1433
DB 2108 ACAGCATGAGGTGTGTGACAGGAGCGAGCGGCCCACTTCCCGAGTTCTCTACTCGG 2167
QY 1434 CAAG 1437
DB 2168 CCAG 2171

RESULT 4
US-09-212-771-1
Sequence 1, Application US/09212771
Patent No. 5958773
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
FILE REFERENCE: RTS-0034
CURRENT APPLICATION NUMBER: US/09/212,771
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2610
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (199)..(1641)
US-09-212-771-1

Query Match 46.5%; Score 719.2; DB 2; Length 2610;
Best Local Similarity 70.3%; Pred. No. 4.3e-206;
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

QY 5 GTCATATGAGCGATGTACCATTTGAAAGAAAGTTGGGTTCAAGAGGGGAGATAT 64
DB 193 GGCACCATAGCGACCTGGCTATTTGAGAGAGGTTGGCTGCACAAAGAGGGGAGTAC 252
QY 65 ATBAAAGCTGAGGCGCAAGATACCTTTTGAAGACAGATGGCTCATTCATAGATAT 124
DB 253 ATCAAGACTTGGGCGGCGCTACTTCTCTCAAGAAATGATGGCACTTCAATGGCTAC 312

QY 125 AAGAGAAACCTCAAGATGTGATTTACTTTA---TCCCTTCAACACTTTTCAAGTGCA 181
DB 313 AAGAGCGGCGCAGAGATGTGGAACAGTAGGCTCCCTTCAACACTTTCTGTGGG 372
QY 182 AATGCGATTAATGAAAAAGAGACCAAGCCAAACACTTTATATCATGATGTCTC 241
DB 373 CAGTCCAGCTGATAGAGCGAGCGGCCCGGCCCAACACTTATCATCTGCTGCTCG 432
QY 242 CAGTGAATCTGTTATAGAGAACTTTTATGATATCTCCAGAGGAAAGAGAA 301
DB 433 CAGTGAACCATCTGTATGAGAGCACTTCCATGTGAGATCTCTGAGAGGGGAGAG 492
QY 302 TGAAGAAAGCTATCAGGCTGTAGCAGACACTGCAAGGCAAGAGAGAGAGATG 361
DB 493 TGAAGAAAGCGCATCAAGCTGTGCTGAGCGGCTCAAGAAAGCAGAGAGAGAGATG 552
QY 362 AATTTGATCCCACTTCAAAATTTATATATAGAGAGAGAGATGATGCTCTTACA 421
DB 553 GACTTCCGGTCCGGGCTCACCAGTGAACCTCAGGGGCTGAGAGATGAGATGTCTCCTG 612
QY 422 ACCCATC---ATBAAAGAAAGCAATGATGATTTTGAATTTTGAATTAATTAAGTAA 478
DB 613 GCCAAGCCCAAGACCGCGTGCATGAGACAGATTTGAGTACTGAGCTGCTGGGCAAG 672
QY 479 GGCACCTTTTGGAAAGTTATTTTGTGAGAGAGAGAGAGAGAGAAATTAATGATG 538
DB 673 GGCACCTTTGCGAAGTATCTGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 732
QY 539 AAGATTTGAGAAAGAAAGTCAATTTGCAAGAGATGAGAGAGAGAGAGAGAGAG 598
DB 733 AAGATCTCAAGAAAGAAAGTCAATTTGCAAGAGAGAGAGAGAGAGAGAGAGAG 792
QY 599 AGCAGAGATTTAAAGAAACATGACATCCCTTTTAAACATCTTGAATATCTTCCAG 658
DB 793 AACCGCTCTGCAAGATCTCAGAGACCCCTTCTCAAGCCCTGAAGTACTTTCCAG 852
QY 659 ACAAAGACCGTTGTGTGTGTGTGATGAGAAATGTAATGAGGAGCGAGCTGTTTCCAT 718
DB 853 ACCCAAGACCGCTCTGCTTTGTCAATGAGATGAGCCAAAGGGGAGAGAGCTGTTCCAC 912
QY 719 TTGTGAGAGAGCGGCTGTTCTTGAAGACCGCAACGTTTCTATGTGAGAAATGTGC 778
DB 913 CTGTCCCGGAAACGTTGTCTTCCAGAGACCGGGGCCCGCTTCTATGTGAGATGTG 972
QY 779 TCTGCTTGAATATATCTATCATTCGCGAAAGAA---TTGTGTACGATCTCAAGTTGGAG 835
DB 973 TAGGCTTGAATATCTATCATTCGCGAAAGAAAGAGAGAGAGAGAGAGAGAGAG 1032
QY 836 AATCTAATGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895
DB 1033 AACTCATGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1092
QY 896 GGGATCAAGATGACAGCCCATGAAAGACATTTCTGTGGCACTCCAGAAATTTGGACCA 955
DB 1093 GGGATCAAG 1152
QY 956 GAGGTGTTAAGATATGACTATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1015
DB 1153 GAGGTGTTAAGATATGACTATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
QY 1076 GAATTAATTAATGAGAGACATTAATTTCTGGAACACTCTCTTCAATGCAAAATCA 1135
DB 1273 GAGCTATCTCATGAGAGAGATCCGCTTCCGCGACAGCTTGTGTCGAGGCGCAAGTCC 1332
QY 1136 TTGCTTTCAAGGCTCTTGTATTAAGAGATCAATTAAGAGAGAGAGAGAGAGAGAG 1195
DB 1333 TTGCTTTCAAGGCTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1392
QY 1196 GCAAAAGAAATTAATGAGACAGATTTCTTCTGAGATTAAGTGGCAAGATGATATGAT 1255

Accession	Sequence	Position
Db	GCACGGAGATCATCAGCATCGCTTTTGGCGGTATCGTGTGCAGCACTGTATCAG	14522
Oy	AAAAAGCTTGTACTCTCTTTTAAACCTCAAGTAACTATGAGACAGATATATATTT	1315
Db	AAGAAGCTCAGCCCACTTCAGGCCCAAGGTCACTGTGAGACTGACACACGGATATTT	1512
Oy	GATGAAGATTTACGCTCAGACTTTTCAATTAACACCACTGAAAAAATATGATAGAGAT	1375
Db	GATGAGAGTTTCACGGCCAGATGATCACTACACCACTGACCAA-----GATGAC	1566
Oy	GGTATGACCTCATGAGCAATGAGAGGGGGCGCATTTCCCTCAATTTTCTACTCTGCA	1435
Db	AGCATATGATGTGTGTGACAGCGAGCGCAGGCCCACTTCCCTCCAGTTCTTACTCGGC	1626
Oy	AGTGCAGCAGATTAATGTC	1453
Db	AGCAGCACGGCCCTGAGGC	1644
Db	AGCAGCACGGCCCTGAGGC	1644

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RESULT 5
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091, 058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

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Query Match	46.5%	Score 719.2	DB 3	Length 2610
Best Local Similarity	70.3%	Pred. No. 4.3e-206		
Matches 1025	Conservative	0	Mismatches 418	Indels 15
			Gaps	4
QY	5	GTGATCATGAGCGAGTTCACATTGTGAAAGAGGTTGGATTCAAGAGGGGAGAAATAT	64	
Db	193	GGCACCAATGAGGAGAGCTGGCTATTGTGAAGAGGGTTGGCTGCACAAACGAGGGAGTAC	252	
QY	65	ATAAAAAACTGGAGGCCAAGATTACTCTCTTTGAAAGACAGATGGCTCATAGATAT	124	
Db	253	ATCAAGACTGGCGGCCACAGCTACTTCTCTCAAGAAATGATGGACCTTATGGCTAC	312	
QY	125	AAAGGAAACCTCAGATGTGTGATTACTTA---TCCCTCCAAACATTTTCAGTGGCA	181	
Db	313	AAGGACGGCGCGCAGAGATGTGGACCAAGGTAGAGCTCCCTTCACAACTTCTGTGTGGC	372	
QY	182	AAATGCGAGTTAATGAAACAGAACGACCAAGCCAAACACATTATATCAGATGTCTC	241	
Db	373	CAGTCCACGCTGATTAAGACGGAGGGGCCCCGGCCAAACACTTCATATCCGCTGCTG	432	
QY	242	CAGTGACTACTGTTATAGAGAAACATTTTCAATGATTACTCCAGAGAAAGGAAAGA	301	
Db	433	CAGTGGACCACTGATCATGAACGACACTTTCATGTGGAAGCTCCGAGAGAGGGGAGAG	492	
QY	302	TGGACAGAAAGCTATTCAGGCTGTAGACAGACGCTGACAGGCGCAAGAAAGAGAGATG	361	
Db	493	TGGACAAACCGGCATTCAGACTGTGTGCTACGGCCCTCAAGAACAGAGAGAGAGAGATG	552	

QY	362	AATTGTAGTCCAACTTTCACAAATTGTAAATATATAGAGAGAGAAAGATNGATGCTCTAC	421
Db	553	GAC TTCGGTCCGGGCTCAACCAGTGAACACTTCAGGGGCTAAGAGATGAGGTGCTCTG	612
QY	422	ACCATC---ATAAAGAAAGACAACTAAATGATTTTGTACATTTTGAACCTAAGTAA	478
Db	613	GCCAAGCCCAAGCACCGCGTGACCATAGAGAGTTTGAATGACTGAAGCTGTGGGAG	672
QY	479	GGCACTTTGGGAAAGTTATTTTGTGTGAGAGAGGCAAGTGGAAATACTATGCTATG	538
Db	673	GGCACTTTCGGCAAGGTGATCTCGTGTAGAGAGAGGCCACAGGCGCTACTAGCCTATG	732
QY	539	AAGATTCTGAAGAAAGAAATGATTTATTTGCAAAAGGATGAATGGGACACACTTAACGAA	598
Db	733	AAGATCTCTGAAGAAAGAAATGATCTGTGCGCAAGAGAGAGGTGGCCACACATCCGAG	792
QY	599	AGCAGAGTATTTAAGAACACTAGACATCCCTTTTAAACATCTTGAATAATTCCTTCAG	658
Db	793	AACGCGGTCTCGAAGACTCCAGGCAACCCCTCTCTCAGACCCCTGAAGTACTCTTTCAG	852
QY	659	ACAAAGACCGTTGT	718
Db	853	ACCCAGACGCGCTCTGTCTGTGTATGAAATAGCGCCAAAGGGGCGAGCTGTCTTCAC	912
QY	719	TTGTGAGAGAGCGGGGTCTCTCGAAGACCGCACAGTTCTATGGTGCAGAAATGTCT	778
Db	913	CTGTCCCGGAGACGTGTCTCTCGAGAGACCGGGCCCGCTTCTATGGCGCTGAGATTGTG	972
QY	779	TCTGCTTGAATATCTTACATTCGGAAGA---TGTGTACCGTGTACTCAAGTTGGAG	835
Db	973	TCAACCTCTGAGCTACCTGCACTCGAAGAAAGACGTGTGTACCGGAGCTCAAGCTGGAG	1032
QY	836	AATCTAATGCTGGAAGAAATGGGCAATPAAAAATTACATTTTGGACTTTCAGAAAG	895
Db	1033	AACCTATGCTGGAAGAGAGCGGCACATTTAAGTACACATTCGGGCTGTGCAAGAG	1092
QY	896	GGGATCA CAGATGCAAGCCACCATGAAAGACATTCGTGGCACTCCAGATATCTGGACCA	955
Db	1093	GGATCAAGAGCGGTGCCACCATGAAAGACCTTTTGGCGGCACACTGAGTACTGAGCCCC	1152
QY	956	GAGGTGTTAAGATTAATGACTATATGTCGCGGAGCAGTAGACTGTGTGGGCTTAAGGGGTGTC	1015
Db	1153	GAGGTGCTGAGGACAAATGACTACGCGCGTGCAGTAGCTGTGTGGGCTGTGGCGTGTCT	1212
QY	1016	ATGATGAAATGATGTGTGGGAGGTACTCTTTCTACACACAGAGACCATGAGAACTTTT	1075
Db	1213	ATGTCAGAGATGATGTGTGGGTGCGCTGCTCTTCTACACACAGACCATGAGAACTTTT	1272
QY	1076	GAATTAATATTATGAGAAACATTTAAATTTTCTTGAAACACTCTCTTCAGATGCAAAATCA	1135
Db	1273	GAGCTCATCTCATTGAGAGAGATCCGCTTCCCGGCAAGCTTGGTCCGAGGGCCAATGCC	1332
QY	1136	TTGCTTTCAGGGCTCTGATTAAGGATTCGAAATTAAGCGCTGTGTGAGAGACAGATGAT	1195
Db	1333	TTGCTTTCAGGGCTCTGATTAAGGAGAACCCAGAGAGGCTGTGTGGGCGCTCGAGGAC	1392
QY	1196	GCAAGAGAAATTAAGACACAGTTTCTTCTGTGAGTAACTGTGCAAGATGTATATGAT	1255
Db	1393	GCAAGAGATCATGACAGCATCGTCTTTTGGCGGTATCGTGTGGCAGCACGTATAGAG	1452
QY	1256	AAAAAGCTTGACTCTCTTTTAAACCTCAAGTAACTGTGAGCAGATACTAATATTTT	1315
Db	1453	AAGAAGCTCAGCCACCTTCAAGCCCAAGTCACTGTGAGACTGACACAGGATATTTT	1512
QY	1316	GATGAAGAATTTACAGCTCAGACTATTAACAATAACACAGCTGAAAAAATATGATGAGAT	1375
Db	1513	GATGAGAGATTCAGCGCCAGATGATACCATACACACTGACCA-----GATGAC	1566
QY	1376	GGTATGACCTGCATGACAAATGAGAGCGGCGCGATTTCTCTCAATTTTCTACTCTGCA	1435
Db	1567	AGCATGAGATGTGTGACAGCGAGCGAGGCGCCACTTCTCCCAAGTCTCTACTCGGCG	1626

QY 1436 AGTGACGAGAAATAGTC 1453
DB 1627 AGCAGCAGCGCTGAGGC 1644

RESULT 6

US-09-023-655-1206

Sequence 1206, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESSES:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1206:

SEQUENCE CHARACTERISTICS:

LENGTH: 2610 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9190827

US-09-023-655-1206

Query Match

Best Local Similarity 46.5%; Score 719.2; DB 4; Length 2610;

Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

QY 5 GTCATATAGAGCATTTTACCATTTGAAAGAAAGTTGGCTTCAGAAAGGGAGCAATAT 64
DB 193 GGCACCATAGAGCACTGGCTATTGGAAGAGGGTTGGCTGCACAAAGAGGGAGTAC 252
QY 65 ATAAAAAATGAGAGGCAAGATATCTCTTTTGAAGACAGATGGCTCATTCAATAGATAT 124
DB 253 ATCAAGACCTGGCGGCAAGCTTCTCTCTTCACAGAAATGATGACCTTTCATTGGCTAC 312
QY 125 AAAGAGAAACCTCAAGATGTGATTTTACCTTA---TCCCTCAACAACCTTTTCAGTGGCA 181
DB 313 AAGAGAGCGGCGGAGAGATGTGACCAACGTGAGGCTCCCTCAACAACCTTCTGTGGCG 372
QY 182 AATAGCAGATTATGAAACAGAAAGCAAGCCCAACATTTTATTCAGATGTCTC 241
DB 373 CAGTGCAGACTGATGAAGACGAGCGGCCGCCCAACACCTTCATTCGCTGCTGG 432

QY 242 CAGTGAAGTACTGTATATAGAGAAACATTTTCATGATTAATCTCAGAGAAAGAAAGAA 301
DB 433 CAGTGAAGTACTGTATATAGAGAAACATTTTCATGATTAATCTCAGAGAAAGAAAGAA 492
QY 302 TGAAGAGAACTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAAAGAGAGAAATG 361
DB 493 TGAAGAGAACTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAAAGAGAGAAATG 552
QY 362 AATTGATGCCAATCTTCACAAATTTGATTAATAGAGAGAAAGAAATGATGATGCTTACA 421
DB 553 GACTTCGGTGGGCTCACCCAGTACAACTCAGGGGCTGAAGAGATGAGGTGCTCCCTG 612
QY 422 ACCCATC---ATAAAGAAAGACATGATGATGATTTTACTATTTGAACTAGATGATAA 478
DB 613 GCCAAGCCCAAGCAGCCGCTGACATGAAAGAGTTGATGATCTAGTACTGCTGGGCAAG 672
QY 479 GGCACCTTTGGAAAGTATTTGGTTGAGAGAAAGCAAGTGAAGAAATCTATGCTATG 538
DB 673 GGCACCTTTGGCAAGTATCTGGTGAAGAGAAAGCCACAGCCGCTACTACGCCATG 732
QY 539 AAGATTCGAAAGAAAGAAAGTCTTATTTGCAAGAGTGAAGTGGCAACACTTAACTGAA 598
DB 733 AAGATTCGAAAGAAAGAAAGTCTTATGTCAGAGAGAGAGTGGCCACACACTCACAG 792
QY 599 AGCAGAGTATTAAGAAACATGACATCCCTTTTAAATCTTGAATATTCCTTCAG 658
DB 793 AACCGGCTCTGCAAACTCCAGAGCAACCTTCTCAGAGCCCTTAAGTACTCTTCCAG 852
QY 659 ACAAAGACCGTTGTGTTTGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTCCAT 718
DB 853 ACCCAGACCGCTCTGCTTTGTGATGAGAGAGCCCAACGGGGGCGAGCTGTTTCCAC 912
QY 719 TTGCGAAGAGCGGGGTCTCTGAGAGACCGGCAACGTTTCTATGTCGAGAAATGTC 778
DB 913 CTGTCCGGGAAACGTTGTTCTCGAGAGACGGGCGCCCTCTTATGTCGAGATGTC 972
QY 779 TCTGCTTGAATATCTATCATTTCCGAAAGAA---TTGTGATCCGATCTCAAGTTGAG 835
DB 973 TCAAGCTCTGACTACTGCACTCGGAGAAAGACGTTGTATCCGGGACCTCAAGCTGAG 1032
QY 836 AATCTAATCTGAGCAAAAGATGCGCAATTAATTAATCAAGATTTTGAATTTGCAAGAA 895
DB 1033 AACTCATGCTGAGCAAGAGCGGCAATTAAGATCAAGACTTGGGGCTGTGCAAGGAG 1092
QY 896 GGGATCAGAGATGACGCAACCATGAAAGATCTGTGCACTCCGAATATCTGACACA 955
DB 1093 GGGATCAGAGATGACGTCACCATGAAAGCTTTTGGGCAACCTGAGTACTGGCCCC 1152
QY 956 GAGGTGTAAGAGATATGATGATGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1015
DB 1153 GAGGTGTAAGAGATATGATGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
QY 1016 ATGTATGAATGATGTGAGAGGTTTACCTTTCTAACAACAGAGCCATGAGAACTTTT 1075
DB 1213 ATGTATGAATGATGTGAGAGGTTTACCTTTCTAACAACAGAGCCATGAGAACTTTT 1272
QY 1076 GATTAATTAATGAGAGACATTAATTTCTGCAACACTCTCTTCAAGTGCAGAAATCA 1135
DB 1273 GAGCTATCTCATGAGAGAGATTCGCTTCCGCGCAAGCTTGTGTCGAGGCAAGTCC 1332
QY 1136 TTGCTTTCAGGCTCTTGTATTAAGATCAATAAAGCCCTTGTGAGAGACCAATGAT 1195
DB 1333 TTGCTTTCAGGCTCTTGTATTAAGATCAATAAAGCCCTTGTGAGAGACCAATGAT 1392
QY 1196 GCAAAAGAAATATGAGACAGATTTCTCTGAGTAAACTGGCAAGATATATGAT 1255
DB 1393 GCAAGAGATATGAGATGAGATTTCTTGTGCGGTATCGTGTGACAGAGTATGACAG 1452
QY 1256 AAAAGCTTGTATCTCTTTTAACTCAAGTAAATCTGAGACAGATATGATATTT 1315
DB 1453 AAGAGCTCAGCCACCTTCAAGGCCAGAGTCAAGTGGAGATGAGACCAAGATATTT 1512

FILE REFERENCE: 3759-0110P
 CURRENT APPLICATION NUMBER: US/09/417,197
 CURRENT FILING DATE: 1999-10-07
 NUMBER OF SEQ ID NOS: 143
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 70
 LENGTH: 2181
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: PKB-EGFP fusion
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(2178)
 US-09-417-197-70

Query Match 46.3%; Score 716.4; DB 4; Length 2181;
 Best Local Similarity 70.7%; Pred. No. 2,7e-205;
 Matches 1015; Conservative 0; Mismatches 406; Indels 15; Gaps 4;

QY 11 ATGAGGATGTTACCACTGTGAAAGAGTTGGGTTCAAGAGAGGGGAGATATATATAA 70
 DB 1 ATGAGGAGCTGCTATGTGTGAAGAGGTGGCTGCACAAAGAGGAGTACATCAAG 60
 QY 71 AACTGAGGCCAAGATCTCTCTTTGAAGAGAGATGGCTCATTTCAATAGATATAAAG 130
 DB 61 AACTGGCGGCCAGCGTACTTCTCTCTCAAGATGATGACCTTCATTGGCTACAAAGAG 120
 QY 131 AAACCTCAAGATGTGATTTACCTTA--TCCCTCAACAACCTTTCACTGGCAAAATGC 187
 DB 121 CGGCGCGAGATGTGACCAAGTGAAGGTGGCTCCCTCAACAACCTTCTGTGGCGAGTGC 180
 QY 188 CAGTTAATGAAACGAAGACCAAGCAAAACCAATTAATATCATGATGTCTCCAGTGG 247
 DB 181 CAGCTGATTAAGCGAGAGGCGCCCGGCCCAACCTTATCATCTCGCTGCGAGTGG 240
 QY 248 ACTACTGTTATAGAGAACATTTCAATGATGATCTCAAGAGAAAGGAGAGATGAGACA 307
 DB 241 ACCACGTGATCGAAGCGACCTTCCATGTGAGAGCTCTGAGAGAGCGGAGAGTGGACA 300
 QY 308 GAACTATCCAGCTGTAGACAGACAGCTGCAAGGCAAGAAAGAGAGAAATGAATTGT 367
 DB 301 ACCGCGATCAACCTGTGCTGACGCGCTCAAGAAAGCAGAGAGAGAGATGACCTTC 360
 QY 368 AGTCCAACTTCAATATGATATATAGAGAGAGAGATGGATGCTCTCAACCCCAT 427
 DB 361 CGGTGGGCTCACCGAGTACCACTCAGGGGCTGAAGAGATGGAGTGTCCCTGGCCAG 420
 QY 428 C--ATMAAAGAAAGCAATGATGATTTTGAATTTGAACTAAGTAAAGGCACT 484
 DB 421 CCCAAGCACCGCGTGAACATGAACAGTTTGAAGTACCTGAAGCTGTGGCAAGGCACT 480
 QY 485 TTTGGAAAGTATTTTGGTTGAGAGAGGCAAGTGGAAATPACTATGCTATGAAGTT 544
 DB 481 TTCGCAGAGTATCTGTGTGAAGAGGAGCCACAGGCGCTACTACCCCATGAGATGC 540
 QY 545 CTGAAGAAAGATGCTATTATGCAAGATGAAGTGGACACACCTTAATCTGAAGCAGA 604
 DB 541 CTCAGAAAGAAAGTCTCTGTGGCAAGAGCAGAGTGGCCCACTACCGAGAACCGC 600
 QY 605 GTATTAAAGACATAGACATCCCTTTTAACTCTTGAATATCTCTTCAGACAAA 664
 DB 601 GTCTGCAAGACTCCAGGACCCCTTCTCAAGCCCTGAAGTACTCTTCCAGAACCG 660
 QY 665 GACCGTTTGTGTGTGATGAAATGTGTAATGGGGGCGAGCTGTTTTCATTGTTG 724
 DB 661 GACCGCTCTGTGTGTGATGAGTACGCAACGCGGGGAGGTGTTCTTCCACCTGTGC 720
 QY 725 AAGAGCGGGTGTCTCTGAGAGCGCAGACGTTTATGAGGCAAGAAATGTCTCTGC 784
 DB 721 CGGGAACGTGTGTCTCTCGAGAGCGGGCCGCTTATGTGGCGCTGAGATGTGTAGCC 780
 QY 785 TTGACTATCTCATTCGGAAGA--TTGTGTACCTGATCTCAAGTTGAGATCTTA 841

DB 781 CTGACCTACCTGCACTCGAGAAAGACGTGGTGTACCGGAGCTCAAGCTGAGAACCTC 840
 QY 842 ATGCTGACAAAGATGGCCACATAAAATTAACAGATTTTGAATTTTGCAGAAAGAGATC 901
 DB 841 ATGCTGACAAAGAGAGGAGCACTTAAGATCAACAGCTTGGGCTGTGACAGAGAGATC 900
 QY 902 ACAGATGAGCCACCATGAAAGACATTTCTGTGCACTCCAGAAATATCTGACCAAGAGTG 961
 DB 901 AAGAGCGTGGCCATGAAAGACCTTTTGGGCAACCTGAATCTTGCCCCCAGAGTG 960
 QY 962 TTGAAGATTAATGACTATAGCCGAGCAGTGAAGCTGGGGCTTGAAGGATGTAT 1021
 DB 961 CTGAGAGCAATGACTAGCGCGTCAAGTGAAGCTGGGGGCTGGGCTGTGATGATAC 1020
 QY 1022 GAAATGATGTGGAGAGTACTTTCTTCAACACCGACCAATGAAACCTTTTGAATTA 1081
 DB 1021 GAGATGATGTGGGCTGCGCTGCTTCAACACCGACCAATGAAAGCTTTTGAAGCTC 1080
 QY 1082 ATATTAAAGAAAGACATTAATTTTCTGAAACACTCTCTTCAGATGCAAAATCATTTGCTT 1141
 DB 1081 ATCTCATGAGAGATCCGCTTCCGCGACAGCTTGGTCCGAGGCCAAGTCTTGCTT 1140
 QY 1142 TCAGGGCTCTTGATTAAGAGATCAAAATAAAGCTTGTGAGAGACAGATGATCAAAA 1201
 DB 1141 TCAGGGCTGCTCAAGAAAGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGAGCGCCAA 1200
 QY 1202 GAAATTAAGACACAGATTTCTCTCTGAGATGAACCTGGCAAGATATATGATAAAG 1261
 DB 1201 GAGATCATGACAGATCGCTTCTTTCGCGTATCGTGTGGCAGACGTGTACAGAAAG 1260
 QY 1262 CTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTGATGA 1321
 DB 1261 CTCAGCCACCTTCAAGCCCAAGTCACTGTGAGATGACACAGATTTTATGAG 1320
 QY 1322 GAATTAAGCTCAGACTATTAATAATTAACCACTGAAATAATGATGAGATGATG 1381
 DB 1321 GAGTCAAGGCCCAAGATATCAATCAACACCACTGACCAA-----GATACAGCATG 1374
 QY 1382 GACTGATGAGCAATGAGAGGGGCGGATTTCCCTCAATTTCTACTCTGCAAG 1437
 DB 1375 GAGTGTGAGACAGAGGAGCGCCCACTTCCCGAGTTCTCTACTCGGCGAG 1430

RESULT 9
 US-09-256-465-1
 Sequence 1, Application US/09256465
 Patent No. 6043090
 GENERAL INFORMATION:
 APPLICANT: Brett P. Monia
 APPLICANT: Lex M. Cowert
 TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
 FILE REFERENCE: RTS-0035
 CURRENT APPLICATION NUMBER: US/09/256,465
 CURRENT FILING DATE: 1999-02-23
 NUMBER OF SEQ ID NOS: 47
 SEQ ID NO 1
 LENGTH: 1599
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (88)..(1533)
 US-09-256-465-1

Query Match 42.5%; Score 658.2; DB 3; Length 1599;
 Best Local Similarity 67.7%; Pred. No. 8.1e-188;
 Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

QY 5 GTATCATGAGCGATGTTACATTTGTGAAGAGTGGGTTCAAGAGGGGAGAAATAT 64
 DB 82 GCCACATGAATGAGAGTGTGTCTATCAAGAAAGGCTGCTCCACAGCGTGTGAATAC 141

QY ATAAAAAAGTGGAGCCAGATCTTCTTTGAAGACAGATGGCTCATTCATAGGATAT 124
DB ATCAAGACTTGGAGCCAGCTTCTTCTTGAAGACGAGCTTCTTCAATGGGTAC 201
QY AAAGAGAACTTGAAGTGTGAATTTACCTTATCCCC--TCAACAATTTTCAAGTGA 181
DB AAAGAGAGGCGCGAGGCGCTGATCAAGCTCTACCCCTTAAACAACCTTCCGTAGCA 261
QY AAATGCCATTATGAAACAGAACGACAAAGCCAAACATTTTATCAGATGCTC 241
DB GAATGCCAGCTGTATGAAGCCGAGAGGCGCGACCCCAACACTTTGTTCATACCTGCTG 321
QY CAGTGGACTCTGTATAGAGAACATTTATGATGATCTCAGAGGAAAGGAAAGAA 301
DB CAGTGGACCACTCATCGAGAGACCTTCCAGTGGATTTCTCAGACGAGAGAGAG 381
QY TGGACAGAACTTATCCAGGCTGTAGACAGACT-----GCAGAGCCAAAGAGAGAG 355
DB TGGATGGGGCCATCCAGATGTGTCCGCAACAGCTCAGAGAGGCGCGCCAGGCGAGAG 441
QY AGAATGAATTTGTATCCAACTTCAAAATTTGATTAATAGAGAGAGAGATGCC 415
DB CCCATGAGACTTCAAGTGTGGCTCCCGAGTGACTCTCCACGACTGAGAGATGAGAGTG 501
QY TCTACAACCAT--CATMAAGAAAGCAATGATGATTTGATCTATTTGAACCTACTA 472
DB GCGGTGAGCAAGGCAAGGCTTAAGTGAATGATGATGATGATGATGATGATGATGATG 561
QY GGTAAAGGCACTTTTGGAAAGTATTTTGTGTGAGAGAGCAAGTGAAGTATCTAT 532
DB GGAAGAGGAACTTTGGCAAGTCACTCTGTGTGGAGAGAGGCACTGGCCGCTACTAC 621
QY GCTATGAAGTTTGAAGAAAGATCATTTTGAAGAGATGAAGTGAAGTGAAGTGA 592
DB GCATGAAGATCTTGGAGAAAGATGATCATTTGCAAGGATGAAGTGCCTCAACAGTGC 681
QY ACTGAAGAGAGATTTAAAGAAACATGAGCATCCCTTTTAACTCTTGAAGTATTC 652
DB ACCGAGAGCGGGTCTTCAAGAACAGGACCCGCTCTCACTGGCTGAAGTATGCC 741
QY TTCAGACAAAGACGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 712
DB TTCACAGCCAGACGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 801
QY TTCATTTTGTGAGAGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 772
DB TTCACCTGTCCGCGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861
QY ATTGTCTGCGCTTGTGATCTATCACTCCGGAAGATTTGTGATCCGTATCTCAAGTTG 832
DB ATTGTCTGCGCTTGTGATCTATCACTCCGGAAGATTTGTGATCCGTATCTCAAGTTG 921
QY GAGATCTATGCTGAGCAAGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTA 892
DB GAAACCTCATGCTGAGCAAGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTA 961
QY GAAAGATCAAGATGAGCAAGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTA 952
DB GAGGAGATCAAGATGAGCAAGATGAGCAATTAATTAATTAATTAATTAATTAATTAATTA 1041
QY CCAAGAGTGTATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1012
DB CCAAGAGTGTATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1101
QY GTCATGATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1072
DB GTCATGATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1161
QY TTTGAATTAATTAATTAATGAAGATTAATTAATTTCTTGAACTCTTCTTCAAGTGA 1132
DB TTTGAATTAATTAATTAATGAAGATTAATTAATTTCTTGAACTCTTCTTCAAGTGA 1221
QY TCAATTCCTTTCAAGGCTTGTGATTAAGATCCAAATTAACGCTTGTGTGAGAGCAAGAT 1192

DB 1222 TCCCTCTGCTGGGCTGTGATTAAGAGACCCCAAGCAAGGCTTGTGTGGGCGCCAGC 1281
QY 1193 GATGCAAAAGAAATTAAGACACAGTTTCTTCTGTGAGTAACTGCGAAGATGATAT 1252
DB 1282 GATGCAAGAGAGATTAAGACACAGTTTCTTCTGTGAGTAACTGCGAAGATGATAT 1341
QY 1253 GATTAAGAGTGTACTCTTCTTAACTCAAGTAACTTGAAGCAATTAATTAATTAAT 1312
DB 1342 CAGAAAGACTCTGACCTTCAAACTCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1401
QY 1313 TTTGATGAAGAAATTAACCTGAGTAACTTAACTCAATCAACCACTGAAATTAATGATGAG 1372
DB 1402 TTGATGATGAATTTTACCGCCAGTCAATCAATCAATCAATCAATCAATCAATCAAT 1455
QY 1373 GATGATGAGTCAATGAGCAATGAGAGGCGCGCATTTCTCTCAATTTCTTACTCTG 1432
DB 1456 GACAGCTGGCTTACTGAGGCTGAGCAAGGCGGACCACTTCCCGAGTTCTCTACTCG 1515
QY 1433 GCAAGTGAACGAGATTAAG 1451
DB 1516 GCCAGCATCCGAGATGAG 1534

RESULT 10

US-09-167-322-3
Sequence 3, Application US/09167322
Patent No. 6365151
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Seidel, Gonda, Lavoigna & Monaco, P.C.
STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-167-322-3

Query Match 42.5%; Score 658.2; DB 3; Length 1599;
Best Local Similarity 67.7%; Pred. No. 8, 1e-188;
Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

5 GTTCATCATGAGGATGTTACATTTGTGAAGAAGGTTGGTTTCAGAGAAGGAGATAT 64
82 GCCACATTAATGAGGTGTCTGTATCAATAAAGAGGTGGCTCCAGAGGTGTGATATC 141
65 ATAAAAATCTGAGGCGCAAGATATCTCTTTGAGACAGATGGCTCATTCATAGATAT 124
142 ATCAAGACTTGAGGCGCAGGTACTTCTGTGAAAGAGGAGCGGCTCTTCAATGGGTAC 201
125 AAGAGAAACCTCAAGATGTGATTTACCTTATCCCC--TCAGAACTTTTCAGTGGCA 181
202 AAGGAGAGGCCCCGAGGCCCTTGATCAGACTTACCCCCCTTAAACAACTTCTCCTAGCA 261
182 AATGCGAGTTATGAAAAAGAGAGCCAAAGCCAAACATTTATTAATCAGATGTCTC 241
262 GAATGCGAGCTGATGAAAGCCAGAGGCGCGCCCAACACCTTTGTCTAGCTGGCTG 321
242 CAGTGAATCTGTTTATAGAGAACTTTCACTGATGATCTCCAGAGAAAGGAGAA 301
322 CAGTGAATCTGATGATGAGAGACCTTCCAGTGTGATTTCTCAGACGAGAGGAGAG 381
302 TGGAGCAAGATCTATCCAGGCTGTAGCAGACACT-----GAGAGGCAAGAGAGAG 355
382 TGAATGCGGCGCATTCAGATGATGCGCAAGCTTCAGAGAGGCGGCCAGCGAGAC 441
356 AGAATGAATTTAGTCCAACTTCAAAATTTGATATATAGAGAGAGAGATGATGCC 415
442 CCATGAGCTACAAAGTGTGGCTCCCGAGTGACTCCTCAAGCTGAGAGATGGAAGT 501
416 TCTACAACTCAT---CATAAAAAGAAAGCAATGATGATTTGACTATTTGAACTACTA 472
502 GCGGTCAGAGAGGAGCGGGCTAAAGGACATGAATGATGATCTGACTATCTCAACCTCT 561
473 GGTAAAGGCACTTTTGGGAAAGTATTTTGTGAGAGAGCAAGGAAATATCTAT 532
562 GCGAAGGAGACCTTTGGCAAAAGTCACTCTGTGCGGAGAAAGGCCACTGCGCTACTAC 621
533 GGTATGAAGATTTCTGAAGAAGAGTCAATTAATGCAAGATGAAGTGCACACTCTA 592
622 GCATGAAATCTCTGGAAGAAGAGTCAATTTGCCAAGATGAAGTGCCTCACACAGTCC 681
593 ACTGAAGAGAGATTTAAAGAAACATACATCCCTTTTAACTCTTGAATTTTC 652
682 ACCGAGAGCGGGTCTCCAGAAACACAGAGACCCGTTCTCTCACTGCTGAAGATGCC 741
653 TTCAGAGCAAAAGACCGTTTGTGTTTGTGATGAGAAATGTTAATGGGCGAGCTGTT 712
742 TTCAGACCCCAAGACCGCTGTGCTTTGTGATGAGATGATGCCAGGGGATGAGCTGTT 801
713 TTCATTTGTGAGAGAGCGGGTGTCTGTAGAGACCGCAACGTTTATGATGTCAGAA 772
802 TTCACCTGTCCCGGAGGCTGCTTCAAGAGAGACCGGCGGTTTATGATGTCAGAG 861
773 ATTGTCTGCTGCTTGTGATCTATCTACATTCGGAAGATTTGTGATCCGTATCTCAAGTTG 832
862 ATTGTCTGCTGCTTGTGATCTATCTACATTCGCGGAGAGTGTATACCGCAATCAAGCTG 921
833 GAGAACTATGCTGAGCAAAAGTGGCAATTAATAATTAAGATTTTGAATTTGGCANA 892
922 GAAAACTATGCTGAGCAAAAGTGGCCATCAATCAATCAATCAATCAATCAATCAAT 981
893 GAAGGATCAAGATGACAGCCACCATGAAGACATTTCTGTGCACTCCAGAAATATCTGCA 952
982 GAGGGCATAGTGAAGCGGGCCACCAATGAAGACCTTGTGAGGACCCCGAGATACCTGGG 1041
953 CAGAGGTTTGAAGAT 1012
1042 CCGAGAGTCTGAGAGACAT 1101
1013 GTCATGTATGAATGATGTGTGAGAGGTTTACCTTTTACAAACAGGAGCATGAAGAACTT 1072
1102 GTCATGTATGAATGATGTGTGAGAGGTTTACCTTTTACAAACAGGAGCATGAAGAACTT 1161
1073 TTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1132

1162 TTGAGCTCATCTCATGGAAGATCGCTTCCGCGCAGCTCAGCCCGAGGCCAAG 1221
1133 TCATGCTTTCAAGGCTCTTGAATAAAGATCCAAATTAAGCTTTGTGAGAGACAGAT 1192
1222 TCCTGCTTGTGAGGCTCTTGAAGAAGACCCCAAGAGAGGCTGTGGGGGGCCAGC 1281
1193 GATGCAAAAGAAATATGAGACAGTTCCTCTGTGAGTAACTGCAAGATGATAT 1252
1282 GATGCCAAGAGATCATGAGACAGGTTCTTCTCAGATCAATGCGCAGAGACCTGATC 1341
1253 GATAAAAAGCTTGAATCTCTTTTAAACCTCAAGTATGAGACAGATATGATAT 1312
1342 CAGAAAGAGCTCTCCACCCCTTCAACCTCAGTCAAGTCCGAGGTGACACAAAGTAC 1401
1313 TTTGATGAAGATTTTACAGCTCAGCTATTAATAAACAACCTGAAAAATATATGAG 1372
1402 TTGATGATGAATTTTACCGCCAGTCAATCAAAATCAACCCCTGACCGCTAT----- 1455
1373 GATGATGAGACTGATGAGACATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCT 1432
1456 GACAGCTGTGCTTACTGAGCTGAGACCAAGCGAGACCACTTCCCACTTCTCTACTG 1515
1433 GCAAGTGAACGAGATTAAG 1451
1516 GCCAGATCCGCGAGTGAAG 1534

RESULT 11
US-09-023-655-1004
Sequence 1004, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1004:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: GENBANK
CLONE: 9178325
US-09-023-655-1004

Query Match 42.5%; Score 658.2; DB 4; Length 1599;
Best Local Similarity 67.7%; Pred. No. 8.1e-188;
Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

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QY 5 GTTATCATGAGCATGTTACCATTTGAAAGAAAGTTGGGTTTCAAGAGAGGAGGAAATAT 64
DB 82 GCCACCATGATAGATGTCCTTCATCAAGAAAGGCTGCTCCACAAGCTGTGTAAATAC 141
QY 65 ATAAAAAAGTGGAGGCAAGATACCTCTTTTGAAGACAGATGGCTCATTCATAGATAT 124
DB 142 ATAAAGCTGGAGGCGACGCTTCTCTCTTAAGAGCGAGCTCTTCAATGGGATAC 201
QY 125 AAGAGAAACCTCAAGATGTGATTTTACCTTATCCC---TCAACAACCTTTTCAGTGGCA 181
DB 202 AAGGAGAGGCGCGAGGCGCTGATCAAGACTCTACCCCTTAACAACCTTCTCGTAGCA 261
QY 182 AATGCCAGTTAATGAAGACAGACCAAGCCCAACATTTATCAGATGCTC 241
DB 262 GAATGCAGCTGTATGAAGACCGAGAGGCGCGACCAACCTTTGTCTATACGCTGCTG 321
QY 242 CAGTGAAGTACTGTATTAAGAGACATTTCAATGATATCTCCAGAGAAAGGAGAA 301
DB 322 CAGTGAAGCAGATGTCATCGAGAGACCTTTCAGTGAATTTCTCAAGACGAGAGAGAG 381
QY 302 TGGACAGAACTATCCAGGCTGTAGCAGACAGACT-----GCAGAGGCAAGAGAGAG 355
DB 382 TGGATCGGGCCATCCAGATGTGTGCGCAACAGCTCAAGAGAGGCGCGCCAGCGAGAGC 441
QY 356 AGAATGAATTTATGTCACACTTCAAAATTGATTAATAGAGAGAGAGATGATGCC 415
DB 442 CCCATGACATCAAGATGTGCTCCCGCAGTACCTCTCCACGACTAGAGAGATGAGATG 501
QY 416 TCTACAACCAT---CATAAAAAGAAAGCAATGATGATTTTACTATTGTAACACTACTA 472
DB 502 GCGGTACAGAGGACGCGCTTAAGTACCATTAATGACTTTCAGATCTCAAACTCTCTT 561
QY 473 GGTAAAGGCACTTTTGGAAAGTATTTTGTTCGAGAGAGGCAAGTGGAAAAATCTAT 532
DB 562 GGGAAAGGAACTTTGGCAAAAGTCATCTGTGTGCGGAGAGAGCCACTGGCCGCTACTAC 621
QY 533 GCTATGAAGTTTGAAGAAAGATCATTTTTCGAAAGATGAAGTGGCACTCTA 592
DB 622 GCCATGAAGATCTTGGAAAGGAGATCATTTGCCAAGATGAAGTGCCTCACACAGTC 681
QY 593 ACTGAAGAGAGATTAATTAAGACACTAGACATCCCTTTTACATCCTTGAATAATTC 652
DB 682 ACCGAGAGCGGGTCTCCAGAAACACAGGACCCGTTCTCACTGCGCTGAAGTATGCC 741
QY 653 TTCACAGCAAAAGACGTTTGTGTGTGTGATGAATATTTATGGGCGGAGCTGTTT 712
DB 742 TTCACAGCCACAGACCGGCTGTGTGTGTGATGAAGTATCCCAACGGGGGTGAGCTGTC 801
QY 713 TTCATTTGTGAGAGAGCGGCTGTCTGAGAGCCGACACGCTTTCTATGTGACAGAA 772
DB 802 TTCACCTGTCCCGGAGCGTGTCTTCAAGAGAGAGCGGCGCGGTTTATGTGACAGAG 861
QY 773 ATTGTCTGCGCTTGTGACTATCTACATTCGCGAAAGATTGTGATCCGTATCTCAAGTG 832
DB 862 ATTGTCTGCGCTTGTGACTATCTGACCTCGGAGAGCTGTATATCCGACATCAAGCTG 921
QY 833 GAGAACTATATGCTGACAAAGATGCGACATATAAAATTCAGATTTTGGACTTTGCAAA 892
DB 922 GAAAACTATATGCTGACAAAGATGCGACATCAAGATCACTGACTTTGGCCTCTGCAAA 961
QY 893 GAAAGGATCAAGATGACGACCATAGAGACATTTCTGTGCACTCCAGAAATCTTGCCA 952
DB 982 GAGGGGATCAGTACGCGGCGACCATGAAACCTTCTGTGAGAGCCCGGAGTACTGGCG 1041
QY 953 CAGAGAGTGTAAAGATTAATGACTATGCGGAGAGTGAAGTGTGGGCGCTTAAGGGGTT 1012

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DB 1042 CCGAGGCTCTGAGAGACAAATGACTATGCGCCGCGCTGAGTGTGGGGCGCTGGTG 1101
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DB 1102 GTCATGTACGATGATGTGTGGCGCGCTGCGCTTCTTACACAGGACCATGAGCGCTTC 1161
QY 1073 TTTGAATTAATTAATGAAGACATTAATTTCCGAAACACTCTCTTCAATGCAAAA 1132
DB 1162 TTCGAGCTCATCTCAATGAGAGATCGCTTCCGCGACGCTCAGCCCGAGGCGAAG 1221
QY 1133 TCATTGCTTTCAGGCTCTTGAATAAGATCCAAATTAACGCTTGTGAGAGACAGAT 1192
DB 1222 TCCCTGCTTCTGCGCTGTGTAAGAGACCCCAAGCAGAGCTTGTGTGGGGCGCCAGC 1281
QY 1193 GATGCAAAAGAAATTAAGACACAGTTCTTCTGTGAGTAACTGCGAAGATGATAT 1252
DB 1282 GATGCCAAGAGATGATGAGACAGGTTCTTCTCAGCATCAACTGGCAGAGCGTGTG 1341
QY 1253 GATAAAAAGCTGTATCTCTTTTAACTCAAGTACATCTGAGACATATCTAGATAT 1312
DB 1342 CAGAAAGCTCTGTGACCTTTCAACCTCAGGTCAAGTCCGAGGTGACACAAAGTAC 1401
QY 1313 TTTGATGAAGATTTACAGCTCAGACTATTAACAATACCACTGAAATAATATGATGAG 1372
DB 1402 TTGATGATGAATTTACCGCCAGTCTCATCAATCAACCCCTGACCGCTAT----- 1455
QY 1373 GATGTATGAGCTGATGAGCAATGAGAGCGCGCGCATTTCTCTCAATTTTCTTACTCT 1432
DB 1456 GACAGCTGAGCTTACTGTGAGCTGAGCAGCGGACCACTTCCCGAGTTCCTTACTCG 1515
QY 1433 GCAAGTGAACGAGATTAAG 1451
DB 1516 GCCAGCATCCGCGAGTGAAG 1534

RESULT 12
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3

Query Match 39.1%; Score 604.4; DB 4; Length 1254;
Best Local Similarity 70.0%; Pred. No. 1.2e-171;
Matches 876; Conservative 0; Mismatches 361; Indels 15; Gaps 4;

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Db      241 CACCGGTACCAATGAACGATTTGAGTACCTGAACCTCTGGGCAAGGCACTTTCCGCG 300
Qy      491 AAAGTATTTTGGTGTGAGAGGAGGCAAGTGAAGAAATGACTATGCTATGAAGATTGGAAG 550
Db      301 AAGGTATCTGTGTGAAGAGGAAGGCA---CAGGCTACTACGCCATGAAGATCCCTCAAG 357
Qy      551 AAAAGATGATTTATTCGAAAGAGTGAAGTGGCACACACTTAACTGAAGACGAGTATTA 610
Db      358 AAGGAAGTATCGTGGCCAAAGGACGAGTGGCCCAACACTCAACGAGAACCGGCTCAG 417
Qy      611 AAGAACTAGACATCCCTTTTAAATCATCTTGAATATTCCTTCAGACAAAGCCGT 670
Db      418 CAGAACTCCAGGACACCCCTTCTCTACTCGCTGAAGTACTTTTCCAGACCCACGACCGC 477
Qy      671 TTGTGTTTTGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTTTCCATTGTCAGAGAG 730
Db      478 CTCTGCTTTGTCAATGAGTACGCGCAACGGGGGCGAGCTGTTTCCACCTGTCCGGGAG 537
Qy      731 CCGGTGTTCTTGAAGACCGCACAGCTTTCTATGTGCAAGAAATGTCTCTGCTTGGAC 790
Db      538 CGTGTGTCGCCGAGGACCGGGCCCGCTTCTATGCGCTGAGATGTGTCAAGCCCTGAC 597
Qy      791 TATCTCATTTCCGGAAGA---TTGTTACCGGTGATCTGAATGGAGAACTGAATGCG 847
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Qy      848 GACAAAGATGCGCACATATAAATTAAGATTTTGAATTTGCAAGAGAGGATCAAGAT 907
Db      658 GACAAAGAGGGGACATTAAGATCAAGACTTGGGCTGTGCAAGAGAGGAGATCAAGAG 717
Qy      908 GCAACCAATGAAGACATTTCTGTGCACTCCAGAAATTTGCGACCAAGAGTGTAAAG 967
Db      718 GGTGCACCATGAAGACCTTTGCGGCAACCTGATACCTGCCCCCAGGGGTGCGAG 777
Qy      968 GATTAATGATATGAGGAGAGAGTGAAGTGTGGGGCTGAGGGGTTGTCAATGATGAAG 1027
Db      778 GACAAATGACTACGGCGGTGAGTGGAGTGGTGGGGCTGGGCTGTGATGACGAGAG 837
Qy      1028 ATGTGTGGAGGTTTACCTTTCTACACACAGACCATGAGAACTTTTGAATTAATTA 1087
Db      838 ATGTGGGTGGCTGCTTCTTCAACACAGACCATGAGAACTTTTGAAGCTCACTC 897
Qy      1088 ATGGAAGACATTAATTTCTGGAACAATCTCTTCAAGATGCAAAATCATTGCTTCA 1147
Db      898 ATGGAAGACATCGCTTCCCGGCAAGCTTGTGCTCCGAGGCCAAAGTCTTGTTCAG 957
Qy      1148 CTCTTGATTAAGGATGCAAAATAAAGCCTTGTGTGAGAGACCAAGTATGCAAAAGAA 1207
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Qy      1208 ATGAGACACAGTTTCTTCTCTGAGTAACTGGCAAGATGATATGATTAAGACTTGA 1267
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Qy      1328 ACAGCTCAGACTTATCAATTAACACACACTGAAATAATGATGAGATGATGAGCTGC 1387
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Qy      1388 ATGACAAATGAGAGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTG 1439
Db      1192 GTGGAAGAGGAGGAGCGCCCACTTCCCAAGTTCTCTACTGCGCCAGCG 1243

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RESULT 13

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US-09-474-922A-1
; Sequence 1, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Bret P. Monia
; APPLICANT: Lex M. Cowert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 1
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-1

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Query Match      26.1%; Score 403; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 3,5e-111;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      29 GTGAAGAAGCTTGGGCTTCAAGAGGGGAGAAATATTAATAAACTGGAGGCCAAGATAC 88
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Qy      89 TTCTTTTGAAGACAGATGGCTCATTCATAGATTAAGAAGAACTCAAGATGTGAT 148
Db      61 TTCTTTTGAAGACAGATGGCTCATTCATAGATTAAGAAGAACTCAAGATGTGAT 120
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Qy      208 CCAAGCCCAACACATTTATATCAAGATGCTCCAGTGAATCTGTTATGAGAGACA 268
Db      181 CCAAGCCCAACACATTTATATCAAGATGCTCCAGTGAATCTGTTATGAGAGACA 240
Qy      269 TTTCAATGATATCTCCAGAGGAAGGAAGATGACAGAACTATCCAGCTGTAGCA 328
Db      241 TTTCAATGATATCTCCAGAGGAAGGAAGATGACAGAACTATCCAGCTGTAGCA 300
Qy      339 GACAGCTGCAAGGCAAGAGAGAGAAATGATTTGATGCAACTTCAAAATTGAT 388
Db      301 GACAGCTGCAAGGCAAGAGAGAGAAATGATTTGATGCAACTTCAAAATTGAT 360
Qy      389 AATATGAGAGAGAGAGATGATGCTCTTACACCCATCATTA 431
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RESULT 14
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Bret P. Monia
; APPLICANT: Lex M. Cowert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2

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Query Match      24.8%; Score 383.8; DB 3; Length 387;
Best Local Similarity 99.5%; Pred. No. 2,1e-105;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Run on: April 13, 2005, 04:09:48 ; Search time 4784 Seconds
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Title: US-09-869-079b-1

Perfect score: 1547

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.4	2811	15	US-10-324-985A-4
2	1537	99.4	2811	19	US-10-753-267-107
3	1364.8	88.2	1570	10	US-09-526-043-1
4	1364.8	88.2	1570	17	US-10-394-568-1
5	843	54.5	2410	9	US-09-771-161A-66
6	751.4	48.6	2626	15	US-10-324-985A-1
7	751.4	48.6	2626	18	US-10-713-678-5
8	751.4	48.6	2626	19	US-10-735-461-20
9	722.4	46.7	2729	19	US-10-895-225A-56
10	722.4	46.7	2729	19	US-10-895-225A-36
11	722.4	46.7	2978	10	US-09-955-999-43

12	721.2	46.6	2184	14	US-10-072-036-138	Sequence 138, App
13	719.2	46.5	2610	9	US-09-970-000-3	Sequence 328, App
14	719.2	46.5	2610	17	US-10-388-263-329	Sequence 1206, App
15	719.2	46.5	2610	17	US-10-641-643-1206	Sequence 1, Appl1
16	719.2	46.5	2610	18	US-10-713-678-1	Sequence 22, Appl1
17	719.2	46.5	2610	19	US-10-735-461-22	Sequence 3, Appl1
18	719.2	46.5	2610	14	US-10-823-433-3	Sequence 70, Appl1
19	716.4	46.3	2181	19	US-10-072-036-70	Sequence 412, App
20	682.2	44.1	1722	18	US-10-322-281-412	Sequence 2, Appl1
21	682.2	44.1	1741	15	US-10-324-985A-2	Sequence 21, Appl1
22	682.2	44.1	1741	15	US-10-735-461-21	Sequence 57, Appl1
23	682.2	44.1	3010	19	US-10-895-225A-57	Sequence 3, Appl1
24	658.2	42.5	1599	17	US-10-324-985A-3	Sequence 1004, App
25	658.2	42.5	1599	17	US-10-641-643-1004	Sequence 254, App
26	658.2	42.5	1715	15	US-10-007-926A-254	Sequence 23, Appl1
27	658.2	42.5	1715	19	US-10-735-461-23	Sequence 415, App
28	655.2	42.4	2562	18	US-10-322-281-415	Sequence 3, Appl1
29	604.4	39.1	1254	18	US-10-713-678-3	Sequence 5, Appl1
30	586.2	37.9	1140	15	US-10-324-985A-5	Sequence 65, Appl1
31	572	37.0	968	9	US-09-771-161A-65	Sequence 994, App
32	515.8	33.3	1854	14	US-10-198-846-984	Sequence 7, Appl1
33	457.2	29.6	3712	18	US-10-473-939-7	Sequence 21419, App
34	443.6	28.7	879	17	US-10-424-539-21419	Sequence 1, Appl1
35	403	26.1	403	15	US-10-168-771-1	Sequence 2, Appl1
36	383.8	24.8	387	15	US-10-168-771-2	Sequence 677, App
37	380.6	24.6	758	9	US-09-910-943-677	Sequence 1423, App
38	274.2	17.7	2391	17	US-10-172-118-1423	Sequence 115, App
39	274.2	17.7	2391	17	US-10-295-027-115	Sequence 1423, App
40	274.2	17.7	2391	17	US-10-342-887-1423	Sequence 3, Appl1
41	274.2	17.7	2391	18	US-10-737-450-3	Sequence 1, Appl1
42	274.2	17.7	2512	9	US-09-784-249-1	Sequence 302, App
43	274.2	17.7	2572	11	US-09-764-875-302	Sequence 148, App
44	274.2	17.7	2702	11	US-09-764-875-148	Sequence 41, Appl1
45	272.6	17.6	3884	18	US-10-755-889-41	

ALIGNMENTS

RESULT 1
US-10-324-985A-4
; Sequence 4, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-biased Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: human
US-10-324-985A-4

Query Match 99.4%; Score 1537; DB 15; Length 2811;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 ATGAGGATGTACCATTTGTGAAGAGTTGGTTCAGAGAAGGAGGAATATATATAA 70
DB 1 ATGAGGATGTACCATTTGTGAAGAGTTGGTTCAGAGAAGGAGGAATATATATAA 60
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DB 61 AACTGAGGCCCAAGATCTCTTTTGAAGACAGATGGCTCATTCATAGAGATATAAGG 120
QY 131 AAACCTCAAGATGTGATTTACCTATCCCTCAACAACTTCCTAGTGCAAAATGCCAG 190

Db 121 AAACCTCAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCCAG 180
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Db 181 TTAATGAAAAGAGAGACGACCAAGCCAAACACTTATATAGATGTCTCCAGTGGACT 240
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Qy 431 AAAAGAGAGACATGATGATTTTGAATAATTTGAAATCTAAGTAAAGGCACTTTTGGG 490
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Qy 671 TTGTGTTTGTATGGAATATGTATATGAGGGGCGAGCTTTTTCATTTGTCGAGAGAG 730
Db 661 TTGTGTTTGTATGGAATATGTATATGAGGGGCGAGCTTTTTCATTTGTCGAGAGAG 720
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Db 781 TATCTACATTCGCGAAAGATGTGTACCGTGTATCTCAAGTTGAGAGATCTAATGCTGAC 840
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Db 841 AAAAGTGGCCACATATAAAATTAACAGTTTTGAATTTGCAAAAGAGGATCAAGATGCA 900
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Db 901 GCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGACCAAGAGGTGTTAGAAAT 960
Qy 971 AATGACTATGCGGAGCAGATGAGCTGTGTGGGGCTTAAAGGGTTGTCAATGTATGAAATGATG 1030
Db 961 AATGACTATGCGGAGCAGATGAGCTGTGTGGGGCTTAAAGGGTTGTCAATGTATGAAATGATG 1020
Qy 1031 TGTGGAGGTACCTTTCTACAAACGAGACATGAGAAAATTTTGAATTAATTAATTAAG 1090
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Qy 1091 GAAGACATTAATTTCTGGAACACTCTTTCAGATGCAAAATCATTTGCTTCAAGGGCTC 1150
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Db 1141 TTGATTAAGAGATCCAAATTAACGCTTGTGTGAGAGACAGATGATGCAAAAGAAATTAAG 1200
Qy 1211 AAGACACAGTTTCTTCTCTGAGATTAACCTGGCAAGATGTATATGATTAAGAAAGCTTGATCCT 1270
Db 1201 AAGACACAGTTTCTTCTCTGAGATTAACCTGGCAAGATGTATATGATTAAGAAAGCTTGATCCT 1260

Qy 1271 CCTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTTATGATGAAGAAATTACA 1330
Db 1261 CCTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTTATGATGAAGAAATTACA 1320
Qy 1331 GCTCAGACTATTTACAAATTAACACACCTGTAATAATATGATGAGATGTATGAGACTGCATG 1390
Db 1321 GCTCAGACTATTTACAAATTAACACACCTGTAATAATATGATGAGATGTATGAGACTGCATG 1380
Qy 1391 GACATGAGAGGCGGCGCATTTTCCCTCAATTTTCTCTGCAAGTGGACGAGAAATTA 1450
Db 1381 GACATGAGAGGCGGCGCATTTTCCCTCAATTTTCTCTGCAAGTGGACGAGAAATTA 1440
Qy 1451 GTCTCTTCAATCTGCTCACTTCACTGATCATCTTCAATTTATTAATGAAATGATTCCTGG 1510
Db 1441 GTCTCTTCAATCTGCTCACTTCACTGATCATCTTCAATTTATTAATGAAATGATTCCTGG 1500
Qy 1511 ACATCACAGTCTTAGCTTTACATACATGACAGGGGCA 1547
Db 1501 ACATCACAGTCTTAGCTTTACATACATGACAGGGGCA 1537

RESULT 2
US-10-753-267-107
; Sequence 107, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-May, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 94662, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; FILE REFERENCE: MP103-0031RMONMIM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 2811
; TYPE: DNA

ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1) ... (1440)
 US-10-753-267-107

Query Match 99.4%; Score 1537; DB 19; Length 2611;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ATGAGCGATGTTACCATTTGTAAGAAGTTGGGTTGAGAGAGGAGGAAATATATATAA 70
 DB 1 ATGAGCGATGTTACCATTTGTAAGAAGTTGGGTTGAGAGAGGAGGAAATATATATAA 60
 QY 71 AACTGAGGCGCAAGATCTTCTTTGAAAGACAGATGCTCATTCATAGATATATAAG 130
 DB 61 AACTGAGGCGCAAGATCTTCTTTGAAAGACAGATGCTCATTCATAGATATATAAG 120
 QY 131 AAACCTCAAGATGTGATTTACCTTATCCCTCAACAACCTTTCACTGGCAAAATGCCAG 190
 DB 121 AAACCTCAAGATGTGATTTACCTTATCCCTCAACAACCTTTCACTGGCAAAATGCCAG 180
 QY 191 TTAATGAAAACAGAACGACCAAGCCAAACATTTATATATAGATGTCTCCAGTGGACT 250
 DB 181 TTAATGAAAACAGAACGACCAAGCCAAACATTTATATATAGATGTCTCCAGTGGACT 240
 QY 251 ACTGTTATAGAGAACATTTCTATGTAGATCTCCAGAGAAAGGAGAAATGACAGAA 310
 DB 241 ACTGTTATAGAGAACATTTCTATGTAGATCTCCAGAGAAAGGAGAAATGACAGAA 300
 QY 311 GCTATCCAGGCTGTAGACAGACAGCTGACAGGCAAGAGAGAGAGAAATGAAATTTAGT 370
 DB 301 GCTATCCAGGCTGTAGACAGACAGCTGACAGGCAAGAGAGAGAAATGAAATTTAGT 360
 QY 371 CCAACTTCACAAATTGATATATAGAGAGAGAGATGATGCTCTCAACCCATCAT 430
 DB 361 CCAACTTCACAAATTGATATATAGAGAGAGAGATGATGCTCTCAACCCATCAT 420
 QY 431 AAAAGAAACAAATGATGATTTTGAATTTGAAATCTATAGATTAAGGCACTTTTGG 490
 DB 421 AAAAGAAACAAATGATGATTTTGAATTTGAAATCTATAGATTAAGGCACTTTTGG 480
 QY 491 AAAGTATTTTGGTGGAGAGAGAGAGGAAATATCTATGCTATGAAATTTCTGAG 550
 DB 481 AAAGTATTTTGGTGGAGAGAGAGGAAATATCTATGCTATGAAATTTCTGAG 540
 QY 551 AAAAGATCATTTTCAAGAGTAAAGTGGACACACTCTAACTGAAAGCAGATTTA 610
 DB 541 AAAAGATCATTTTCAAGAGTAAAGTGGACACACTCTAACTGAAAGCAGATTTA 600
 QY 611 AAAGACATGACATCCCTTTTAAACATCCTTGAATATCTCTCCAGACAAAGACGT 670
 DB 601 AAAGACATGACATCCCTTTTAAACATCCTTGAATATCTCTCCAGACAAAGACGT 660
 QY 671 TTGTGTTTGTATGTAATATGTAATGGGGGAGACTGTTTTCATTTTGTGAGAG 730
 DB 661 TTGTGTTTGTATGTAATATGTAATGGGGGAGACTGTTTTCATTTTGTGAGAG 720
 QY 731 CCGGTTTCTGTAGAGACCGACACAGTTTCTATGTGAGAAATTTCTCTGCTTGAC 790
 DB 721 CCGGTTTCTGTAGAGACCGACACAGTTTCTATGTGAGAAATTTCTCTGCTTGAC 780
 QY 791 TATCTACATTCGGAAGATTTGTACCGGTATCTCAAGTTGAGAAATCTAATGCTGAC 850
 DB 781 TATCTACATTCGGAAGATTTGTACCGGTATCTCAAGTTGAGAAATCTAATGCTGAC 840
 QY 851 AAAGATGGCCAAATTAATTAAGATTTTGAATTTTGAAGAGAGATCAAGATGGA 910
 DB 841 AAAGATGGCCAAATTAATTAAGATTTTGAATTTTGAAGAGAGATCAAGATGGA 900
 QY 911 GCCACCATGAAGATTTCTGTGAGACTCCAGATATCTGAGCACAAGGTTTGAAGAT 970
 DB 901 GCCACCATGAAGATTTCTGTGAGACTCCAGATATCTGAGCACAAGGTTTGAAGAT 960

QY 971 AATGACTATGGCCGACAGTACATGTCGGGGCTAGGGCTTGATGTAAGAAATGAG 1030
 DB 961 AATGACTATGGCCGACAGTACATGTCGGGGCTAGGGCTTGATGTAAGAAATGAG 1020
 QY 1031 TGTGGAGGTTACCTTTCTACACACAGGACATGAGAAACCTTTGAATTAATTAATG 1090
 DB 1021 TGTGGAGGTTACCTTTCTACACACAGGACATGAGAAACCTTTGAATTAATTAATG 1080
 QY 1091 GAAGCATTAATTTCTTGAAACATCTCTTCAATGCAAAATCATTTGCTTCAAGGCTC 1150
 DB 1081 GAAGCATTAATTTCTTGAAACATCTCTTCAATGCAAAATCATTTGCTTCAAGGCTC 1140
 QY 1151 TTGATTAAGATCCAAATTAAGCTTGGTGAAGACCAAGATGAGCAAAATTAATG 1210
 DB 1141 TTGATTAAGATCCAAATTAAGCTTGGTGAAGACCAAGATGAGCAAAATTAATG 1200
 QY 1211 AGACACAGTTTCTCTGTGAGTAACTGGCAAGATGTATATGATTAAGAAATTTAGCT 1270
 DB 1201 AGACACAGTTTCTCTGTGAGTAACTGGCAAGATGTATATGATTAAGAAATTTAGCT 1260
 QY 1271 CCTTTAAACCTCAAGTAAACATCTGAGACAGATTAATTTGATGAAATTTTACA 1330
 DB 1261 CCTTTAAACCTCAAGTAAACATCTGAGACAGATTAATTTGATGAAATTTTACA 1320
 QY 1331 GCTCAGACTTTACAAATTAACACCACTGAAATATAGATGAGATGTATGACTGCAATG 1390
 DB 1321 GCTCAGACTTTACAAATTAACACCACTGAAATATAGATGAGATGTATGACTGCAATG 1380
 QY 1391 GACAAATGAGAGGCGGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGAAGAAATTA 1450
 DB 1381 GACAAATGAGAGGCGGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGAAGAAATTA 1440
 QY 1451 GTCTCTTCAATCTGCTACTCTGCTACATCTTCAATTTTACTGAAATGATTTCTG 1510
 DB 1441 GTCTCTTCAATCTGCTACTCTGCTACATCTTCAATTTTACTGAAATGATTTCTG 1500
 QY 1511 ACATCACCACTGCTTACTTCTTACATGACATGACAGGGGCA 1547
 DB 1501 ACATCACCACTGCTTACTTCTTACATGACATGACAGGGGCA 1537

RESULT 3

US-09-526-043-1
 ; Sequence 1, Application US/09526043
 ; Publication No. US20030100049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Kun
 ; APPLICANT: Pagnoni, Marco
 ; APPLICANT: Clark, Kenneth
 ; APPLICANT: Ivaschenko, Yuri
 ; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
 ; FILE REFERENCE: A3278A-US
 ; CURRENT APPLICATION NUMBER: US/09/526,043
 ; EARLIER FILING DATE: 2000-03-14
 ; EARLIER APPLICATION NUMBER: 60/125,108
 ; EARLIER FILING DATE: 1999-03-19
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1570
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (126) .. (1523)
 US-09-526-043-1

Query Match 88.2%; Score 1364.8; DB 10; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 1 GGGAGTCATCATGACGAGATGTACATCTGTGTAAGAAGTTGGGTTGAGAAAGGGGAGA 60

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Db      116 GGGAGCATCATGAGGATGTTACCATGTGAAAAGAGGTGGGTTCAAGAGGGGAGA 175
Qy      61 AATATATAAACTGGAGGCCAAGATACCTCTTTGGAAGACAGATGGCTCATTAAG 120
Db      176 AATATATAAACTGGAGGCCAAGATACCTCTTTGGAAGACAGATGGGCTCATTAAG 235
Qy      121 AATATAAGAAACCTCAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGC 180
Db      236 AATATAAGAAACCTCAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGC 295
Qy      181 AAAATGCCAGTTAATGAAAAAGAACGACCAAGGCCAAACACATTTAATCAGATGTCT 240
Db      296 AAAATGCCAGTTAATGAAAAAGAACGACCAAGGCCAAACACATTTAATCAGATGTCT 355
Qy      241 CCAAGTGACTACTGTTATAGAGAGACATTTTCAATGATGATCTCCAGAGAAAGGAAA 300
Db      356 CCAAGTGACTACTGTTATAGAGAGACATTTTCAATGATGATCTCCAGAGAAAGGAAA 415
Qy      301 ATGACAGAGGCTATCCAGGCTGTAGCAGACAGACTCAGAGGCAAGAGAGAGAGAT 360
Db      416 ATGACAGAGGCTATCCAGGCTGTAGCAGACAGACTCAGAGGCAAGAGAGAGAT 475
Qy      361 GAATGTAGTCCAACCTTCACAATTTGATATATAGAGAGAGAGAGATGCTCTTAC 420
Db      476 GAATGTAGTCCAACCTTCACAATTTGATATATAGAGAGAGAGATGCTCTTAC 535
Qy      421 AACCCATCTAATAAGAAACAAATGATTTGACTTTTGAATCTTCTAGTAAAG 480
Db      536 AACCCATCTAATAAGAAACAAATGATTTGACTTTTGAATCTTCTAGTAAAG 595
Qy      481 CACTTTGGGAAAGTATTTGGTTGAGAGAAAGCAAGTGGAAATACTATGCTATGAA 540
Db      596 CACTTTGGGAAAGTATTTGGTTGAGAGAAAGCAAGTGGAAATACTATGCTATGAA 655
Qy      541 GATTCGAGAAAGAGATCATTTTGCAGAAAGATGAAGTGGCAACACTCTTAACTGAAG 600
Db      656 GATTCGAGAAAGAGATCATTTTGCAGAAAGATGAAGTGGCAACACTCTTAACTGAAG 715
Qy      601 CAGAGATTAAGAAACATGACATCCCTTTTAAATCCCTTGAATATTTCTTCCAGAC 660
Db      716 CAGAGATTAAGAAACATGACATCCCTTTTAAATCCCTTGAATATTTCTTCCAGAC 775
Qy      661 AAAAGACGTTTGTGTTTGTGATGAGATATGTAATGGGGCGAGCTGTTTTCCATT 720
Db      776 AAAAGACGTTTGTGTTTGTGATGAGATATGTAATGGGGCGAGCTGTTTTCCATT 835
Qy      721 GTGAGAGAGCGGGTGTCTCTGAGGACCGCAACGTTTCTATGTGAGAAATGTCTC 780
Db      836 GTGAGAGAGCGGGTGTCTCTGAGGACCGCAACGTTTCTATGTGAGAAATGTCTC 895
Qy      781 TGCCTTGGACTATCTATCATTTCCGAGAAAGTGTGATCCGTGATCTCAAGTTGAGATCT 955
Db      896 TGCCTTGGACTATCTATCATTTCCGAGAAAGTGTGATCCGTGATCTCAAGTTGAGATCT 955
Qy      841 AATGTGACCAAGATGCGCACAATAAAATTAACAATTTTGAAGCTTTTGAAGAGAT 900
Db      956 AATGTGACCAAGATGCGCACAATAAAATTAACAATTTTGAAGCTTTTGAAGAGAT 1015
Qy      901 CACAGATGACCAACCATGAAAGACATTTCTGTGGCACTCAGAAATCTTGGCAACAGAGT 960
Db      1016 CACAGATGACCAACCATGAAAGACATTTCTGTGGCACTCAGAAATCTTGGCAACAGAGT 1075
Qy      961 GTTAGAAGATATGACTATGCGCGAGCAATGATGCTGTGGGGCTTATGATGTA 1020
Db      1076 GTTAGAAGATATGACTATGCGCGAGCAATGATGCTGTGGGGCTTATGATGTA 1135
Qy      1021 TGAATATGATGTGGAGGTTACCTTTCTACAAACGAGACCATGAGAACTTTTGAAT 1080
Db      1136 TGAATATGATGTGGAGGTTACCTTTCTACAAACGAGACCATGAGAACTTTTGAAT 1195
Qy      1081 AATATTATGAGAGACATTTAAATTTCTCGAAACACTCTCTTCAAGATGCAAAATCATTGTCT 1140

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Db      1196 AATATTATGAGAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTGTCT 1255
Qy      1141 TTCAGGGCTCTTGAATTAAGAGATCCAAATTAACGCTGTGGAGGACAGATGATGCAA 1200
Db      1256 TTCAGGGCTCTTGAATTAAGAGATCCAAATTAACGCTGTGGAGGACAGATGATGCAA 1315
Qy      1201 AGAAATTAAGAGACAGATTTCTTCTCTGAGTAACTGCAAGATGTAATGATTAATAA 1260
Db      1316 AGAAATTAAGAGACAGATTTCTTCTCTGAGTAACTGCAAGATGTAATGATTAATAA 1375
Qy      1261 GCTTGACTCTCTTTAAACCTCAAGTAACATCTGAGACAGATTAATTTTGAATGA 1320
Db      1376 GCTTGACTCTCTTTAAACCTCAAGTAACATCTGAGACAGATTAATTTTGAATGA 1435
Qy      1321 AGAATTTACGCTGAGCTAATTAACAATTAACAACCTGAAATAATGATGAGATGTAT 1380
Db      1436 AGAATTTACGCTGAGCTAATTAACAATTAACAACCTGAAATAATGATGAGATGTAT 1495
Qy      1381 GGAATGACATGACAAATGAGA 1400
Db      1496 TGGCATGCTGGGTAACTGGA 1515

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RESULT 4
US-10-394-568-1
; Sequence 1, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: IVASHCHENKO, YURI
; TITLE OF INVENTION: CLARK, KENNETH L.
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; FILE REFERENCE: A3399W0
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126) .. (1523)
US-10-394-568-1

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Query Match 88.2%; Score 1364.8; DB 17; Length 1570;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy      1 GGGAGTCATCATGAGCGATGTTACCATTTGTGAAGAGGTTGGTTCAAGAGGGGAGA 60
Db      116 GGGAGTCATCATGAGCGATGTTACCATTTGTGAAGAGGTTGGTTCAAGAGGGGAGA 175
Qy      61 AATATATAAACTGGAGGCCAAGATACCTCTTTGGAAGACAGATGGCTCATTAAG 120
Db      176 AATATATAAACTGGAGGCCAAGATACCTCTTTGGAAGACAGATGGGCTCATTAAG 235
Qy      121 AATATAAGAAACCTCAGATGTGATTTACCTTATCCCTCAACACTTTTCAAGTGGC 180
Db      236 AATATAAGAAACCTCAGATGTGATTTACCTTATCCCTCAACACTTTTCAAGTGGC 295
Qy      181 AAAATGCCAGTTAATGAAAAAGAACGACCAAGGCCAAACACATTTAATCAGATGTCT 240
Db      296 AAAATGCCAGTTAATGAAAAAGAACGACCAAGGCCAAACACATTTAATCAGATGTCT 355
Qy      241 CCAAGTGACTACTGTTATAGAGAGACATTTTCAATGATGATCTCCAGAGAAAGGAAA 300
Db      356 CCAAGTGACTACTGTTATAGAGAGACATTTTCAATGATGATCTCCAGAGAAAGGAAA 415

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OY	360	1	ATGGACAGAGCTATCCAGGCTGTGTGACAGACAGCTGCAGAGCCAAAGAGAGGAAAT	360
Db	475	416	ATGGACAGAGAGCTATCCAGGCTGTGTGACAGACAGCTGCAGAGCCAAAGAGAGGAAAT	475
OY	420	361	GAATGTAGTCCAACTTCCAAATTTGATATATATAGAGAGGAAGAGATGATGCTCTAC	420
Db	535	476	GAAATGTAGTCCAACTTCCAAATTTGATATATATAGAGAGGAAGAGATGATGCTCTAC	535
OY	480	421	AACCATCATAAAGAAAGACAAATGATATTTGACTATTTGAAACTACATGATGAAG	480
Db	595	536	AACCATCATAAAGAAAGACAAATGATATTTGACTATTTGAAACTACATGATGAAG	595
OY	540	481	CACCTTTGGGAAAGTTATTTGGTTCGAGAGAAAGCAACGTGAAATATCTATGCTATGA	540
Db	655	596	CACCTTTGGGAAAGTTATTTGGTTCGAGAGAAAGCAACGTGAAATATCTATGATGA	655
OY	600	541	GATTCGAAAGAAAGATCATTATTGCAAAAGATGAATGGCACAACCTCTAACTGAAAG	600
Db	715	656	GATTCGAAAGAAAGATCATTATTGCAAAAGATGAATGGCACAACCTCTAACTGAAAG	715
OY	660	601	CAGAGTATTTAAAGAACCTAGACATCCCTTTTAACTCCCTTGAAATATTCCTCCAGAC	660
Db	775	716	CAGAGTATTTAAAGAACCTAGACATCCCTTTTAACTCCCTTGAAATATTCCTCCAGAC	775
OY	720	661	AAAAGACCGTTGTGTTTGTGTATGGAATATGTATATGGGGGAGACCTGTTTCCATT	720
Db	835	776	AAAAGACCGTTGTGTTTGTGTATGGAATATGTATATGGGGGAGACCTGTTTCCATT	835
OY	780	721	GTCGAGAGAGCGGAGTCTCTCGAGAGACCGCACACGTTTCTATATGTCGAGAAATGTCTC	780
Db	895	836	GTCGAGAGAGCGGAGTCTCTCGAGAGACCGCACACGTTTCTATATGTCGAGAAATGTCTC	895
OY	840	781	TGCTTGGACTATCTACATTCGGAAGAAAGTTGTATCCGTATCTCAAGTTGGAGATCT	840
Db	955	896	TGCTTGGACTATCTACATTCGGAAGAAAGTTGTATCCGTATCTCAAGTTGGAGATCT	955
OY	900	841	AATGCTGGAACAAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCCAAGAGGAT	900
Db	101	956	AATGCTGGAACAAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCCAAGAGGAT	101
OY	960	901	CACAGATGCAGCCACATAGAGCATTCGTGGCACTCCAGAAATATCTGGCACACAGAGT	960
Db	107	1016	CACAGATGCAGCCACATAGAGCATTCGTGGCACTCCAGAAATATCTGGCACACAGAGT	107
OY	102	961	GTTAGAGATTAATGACTATGCGCGAGACAGTAGACTGTGGGCTTAGGGGTGTCTATGTA	102
Db	113	1076	GTTAGAGATTAATGACTATGCGCGAGACAGTAGACTGTGGGCTTAGGGGTGTCTATGTA	113
OY	108	1021	TGAATATGATGTGGGAGGTTACCTTTCTACAAACAGACCATGAGAACTTTTGAATT	108
Db	119	1136	TGAATATGATGTGGGAGGTTACCTTTCTACAAACAGACCATGAGAACTTTTGAATT	119
OY	114	1081	AATATTAATGAAGAAGCATTAATTTCTCGAAACACTCTCTCGATGAGCAAAATCATGTCT	114
Db	125	1196	AATATTAATGAAGAAGCATTAATTTCTCGAAACACTCTCTCGATGAGCAAAATCATGTCT	125
OY	120	1141	TTCAAGGGCTCTTGATTAAGAGATCCAAATTAACCGCTTGTGTGAGGACAGATGATCAAA	120
Db	131	1256	TTCAAGGGCTCTTGATTAAGAGATCCAAATTAACCGCTTGTGTGAGGACAGATGATCAAA	131
OY	126	1201	AGAAATTTATGAGACACAGTTTCTTCTCTGAGATTAACCTGGCAAGATGATATGAATAA	126
Db	137	1316	AGAAATTTATGAGACACAGTTTCTTCTCTGAGATTAACCTGGCAAGATGATATGAATAA	137
OY	132	1261	GCTTGACCTCGTTTAAACCTCAAGTAAACATCTGAGACAGATCACTAGATATTTGATGA	132
Db	143	1376	GCTTGACCTCGTTTAAACCTCAAGTAAACATCTGAGACAGATCACTAGATATTTGATGA	143
OY	138	1321	AGAAATTTACAGCTCAGACTATTACAAATTAACCACTCTGAAAAATATGATGAGATGAT	138
Db	149	1436	AGAAATTTACAGCTCAGACTATTACAAATTAACCACTCTGAAAAATGTCAGAAATCAATGG	149
OY	1400	1381	GGACTGCATGACATGAGA 1400	

Db	1496	TGCGATGCTGGCTAACTGGA	1515
Db	1496	TGCGATGCTGGCTAACTGGA	1515

Db 912 CTAGATATTTTATGTAAGAAATTTACAGCTCAGACTTATCAATTAACACACCACTGAAAAAT 971
QY 1365 AAGTAGAGATGTATGTATGATCTGATGAGAAATGAGAGGGGCGGCTTTCCCTCAATTTT 1424
Db 972 AATGAATGAGATGTATGTATGATCTGATGAGAAATGAGAGGGGCGGCTTTCCCTCAATTTT 1031
QY 1425 CCTACTCTGATGAGAGAGATAGTCTCTTTCTGCTACTTCACTGCTCAATCTTC 1484
Db 1032 CCTACTCTGATGAGAGAGATAGTCTCTTTCTGCTACTTCACTGCTCAATCTTC 1091
QY 1485 AATTTATTTCTGAAAAATGATTCCTGAGACATCAACAGTCTAGCTCTTACATAGCAGG 1544
Db 1092 AATTTATTTCTGAAAAATGATTCCTGAGACATCAACAGTCTAGCTCTTACATAGCAGG 1151
QY 1545 GCA 1547
Db 1152 GCA 1154

RESULT 6
US-10-324-985A-1
Sequence 1, Application US/10324985A
Publication No. US20030144204A1
GENERAL INFORMATION:
APPLICANT: Spencer, David
TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REFERENCE: P02248US1/10106761
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,155
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2626
TYPE: DNA
ORGANISM: mouse
US-10-324-985A-1

Query Match 48.6%; Score 751.4; DB 15; Length 2626;
Best Local Similarity 71.8%; Pred. No. 2.3e-190;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

QY 8 ATCATGAGGATGTATGATCAATTTGAAAGAGTGGCTCAGAGAGGGAGAAATATATA 67
Db 281 ACCATGAAAGCATGATGACCTTTGTGAAGAGGCTGCTCAACAGAGGGAATATATT 340
QY 68 AAAAATGAGGCAAGATATCTCTTTTGAAGACAGATGCTCATTTAGATATATA 127
Db 341 AAAAATGAGGCAAGATATCTCTTTTGAAGAGGCTGCTCAACAGAGGGAATATATT 400
QY 128 GAGAAATCTCAAGATGTGAT--TTACTTATCCCTCAACAACTTTTCAAGTGGCAAA 184
Db 401 GAAAGGCTCAGAGATGTGATCAGCAGAGATCCCACTCAACAACTTTTCAAGTGGCAAA 460
QY 185 TSCGATTTATGAAAAAG 244
Db 461 TSCGATTTATGAAAAAG 520
QY 245 TGAAGTACTGTTATAGAGAAATTTCTATGATATCTCAGAGAGAGAGAGAGAGAGAGAGAG 304
Db 521 TGAAGTACTGTTATAGAGAAATTTCTATGATATCTCAGAGAGAGAGAGAGAGAGAGAGAG 580
QY 305 AAGAGAGCTATCCAGGCTGTAGACAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 581 GCAAGCAGCTATCAGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
QY 365 TGTAGTCAATTTCAATTTGATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
Db 641 TTTCCGATCGGCTCACCCAGTGAACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
QY 425 CATC--ATAAAAAGAAAGCAATGATGATTTTGAATTTGAACTATTTGAACTAGATAAGGC 481

Db 701 AAGCCAAAGCACCGGTGATCAGATGAAAGAGATTGAGTACTGAACTACTGAGGCAAGGCG 760
QY 482 ACTTTTGGAGAAATATTTTGGTTGAGAGAAAGGCAAGTGAATAATATCTATGTAGAG 541
Db 761 AACTTTGGAGAAATATTTTGGTTGAGAGAAAGGCAAGGCGGCTACTATGATGCAAGAG 820
QY 542 ATTCTGAAGAAAGAGATGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
Db 821 ATCTCAAGAGAGAGATGATGCTGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 880
QY 602 AAGATTTAAAGACATGAGACATCTTTTAAATCTTGAATCTTGAATTTCTTCAAGACA 661
Db 881 CGTGTCTGAGAAATCTAGAGCATCTTCTTCAAGGCGCTTCAAGTACTATTTCAAGACC 940
QY 662 AAAAGCCGTTGTGTTTGTGATGGAATATGTTATGAGGGGAGAGAGAGAGAGAGAGAG 721
Db 941 CAGAGCCGCTTGTGTTTGTGATGGAATATGTTATGAGGGGAGAGAGAGAGAGAGAGAG 1000
QY 722 TCGAGAGAGCGGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
Db 1001 TCTGAGAGAGCGGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1060
QY 782 GCTTGAAGTATCTAATTCGGAAGA--TTGTGTAACGTGATCTCAAGTTGAGAGAT 838
Db 1061 GCCCTGAGACTACTTCACTCCGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1120
QY 839 CTAAATGCTGAGCAAGAGATGCGCAATAAATTTAAGATTTTGAATTTTGAATTTTGA 898
Db 1121 CTGATGCTGAGCAAG 1180
QY 899 ATCAGAGATGAG 958
Db 1181 ATCAGAGATGAG 1240
QY 959 GTTTAAGAGATATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018
Db 1241 GTGCTGAG 1300
QY 1019 TATGAAG 1078
Db 1301 TATGAAG 1360
QY 1079 TTAATATTTAATGAG 1138
Db 1361 CTGATCTCATGAG 1420
QY 1139 CTTTCAAGGCTCTTGAATAAAGAGATCAATTAACAGCTTTGTGAGAGAGAGAGAGAG 1198
Db 1421 CTCTCGGAGTGTCTCAAG 1480
QY 1199 AAAAGAAATTAAG 1258
Db 1481 AAGAGAGATCAAG 1540
QY 1259 AAGCTTTGATCTCTTTTAAACCTCAAGTAAATCTGAGAGAGAGAGAGAGAGAGAGAG 1318
Db 1541 AAGCTGAG 1600
QY 1379 ATGAGCTGATGAG 1438
Db 1655 ATGAGAGTGTGAG 1714
QY 1439 GAGAGAGATTAAGTC 1453
Db 1715 GAGAGAGCTTAAGGC 1729

RESULT 7


```

US-10-713-678-5
; Sequence 5, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10/713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-713-678-5

Query Match      48.6%; Score 751.4; DB 18; Length 2626;
Best Local Similarity 71.8%; Pred. No. 2.3e-190;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

QY      8 ATCATGAGCATGTTTACCATTTGGAAGAAAGTTGGGTTGAGAAAGAGGAGAAATATATTA 67
|      |
DB      281 ACCATGAAACGACATGACATTTGTAAGAGGAGGCTGGTCACAAACGAGGGAATATATTT 340
|      |
QY      68 AAAAATGAGAGGCAAGATATCTCTTTTGAAGACAGATGGCTCATTCATAGGATATTA 127
|      |
DB      341 AAAACGTGGGGGCGACGCTATCTTCTCTCAAGACGATGACCTTTATTTGGCTACAG 400
|      |
QY      128 GAGAAACCTTCAGATGTGAT---TTACCTTATCCCTCAACAACCTTTTCACTGAGCA 184
|      |
DB      401 GAACGCGCTTCAGATGTGATGATCAGCAGAGAGTCCCACTCAACAACCTTCAGTGGCA 460
|      |
QY      185 TGCCATTTATGAAAACAGAAAGCAACAAAGCCAAACATTTTATCATGATGTTCCAG 244
|      |
DB      461 TGCCACCTGATGAAAGACAGAGCGCCCAAGGCCCAACCTTTATCTCCGCTCCGAC 520
|      |
QY      245 TGCACTACTGTTTATGAGAAACATTTCTGATGATCTCAGAGGAAAGGAAAGATG 304
|      |
DB      521 TGGAACAACATCTTTAGAGCGCACTTCTCAATGGAACGCTTGAAGCGGGAAGATG 580
|      |
QY      305 ACAGAACTATCCAGGCTGTAGCAGACAGCTCAGAGGCGAAGAGAGAGAGATGAAT 364
|      |
DB      581 GCCACCGCCATTCAGACTGTGCGCATGACTCAAGAGGCGAGAAAGAGACGATGGAC 640
|      |
QY      365 TGTATGTCCACTTCAAAATTTGATATATGAGAGAGAGATGATGCTCTTACAACT 424
|      |
DB      641 TTCCGATCAGGCTCACCCAGTGACAACTCAGGGCTGAAAGATGAGTGGTCCCTGGCC 700
|      |
QY      425 CATC---ATPAAAGAAAGCAATGATGATTTTGAATTTTGAATTTGAATTTGAATTTGA 481
|      |
DB      701 AAGCCCAAGACCGTGTGACATGAAAGAGATTTGAATTTGAATTTGAATTTGAATTTGA 760
|      |
QY      482 ACTTTTGGAAAGTTATTTTGTTCAGAGAAAGCAAGTGAATAATATATGCTATGAAG 541
|      |
DB      761 ACCTTTGGAAAGTATTTGTTGTAAGAAAGAGGCGACAGGCGGCTATATGCAATGA 820
|      |
QY      542 ATTCTGAAGAAAGATCATTTATTTGCAAGAGATGAAGTGGCACAACCTTAACTGAAG 601
|      |
DB      821 ATCTCTAAGAAAGAGTCAATCGTGGCAAGAGATGAGTTGCCACACGCTTACTGAGAC 880
|      |
QY      602 AGAGATTTAAAGAACTAGACATCCCTTTTAAACATCTTTGAATTTTGAATTTTGAATTT 661
|      |
DB      881 CGGTCTCTGAGAACTTAGGCACTCCCTTCTTACGCGCTCAAGTATCATATTCAGACC 940
|      |
QY      662 AAAGACCGTTTGTGTTTGTATGATGATATGTTAATGGGGCGAGCTGTTTTCATTTG 721
|      |
DB      941 CACGACCGCTCTGCTTTGTGATGATGATGATGCAACGAGGCGAGCTCTTCTTCAACCTG 1000

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QY      722 TCGAGAGAGCGGGTGTCTCTGAGACCGACACGCTTTCTATGATGATGATGATGATG 781
|      |
DB      1001 TCTGAGAGAGCGGTGTCTCTGAGACCGGCGCCGCTTCTATGATGATGATGATGATG 1060
|      |
QY      782 GCTTGGATCTATCTATCATTTCCGAAAGA---TTGTATCCGTGATCTCAAGTTGAGAA 838
|      |
DB      1061 GCGCTGATCTATCTGATCTCCGAAAGAAAGTGTGTATCCGGAAGCTGAAAGCTGAGAAC 1120
|      |
QY      839 CTATGCTGAGCAAGATGCGCACATPAAATTTACATTTTGAATTTGCACTTTGCAAGAG 898
|      |
DB      1121 CTATGCTGAGCAAGATGCGCACATPAAATTTACATTTTGAATTTGCACTTTGCAAGAG 1180
|      |
QY      899 ATCAGAGATGCGCACATPAAATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 958
|      |
DB      1181 ATCAGAGATGCGCACATPAAATTTGAGATTTGAGATTTGAGATTTGAGATTTGAGAT 1240
|      |
QY      959 GTGTTAAGATATATGATCTATGAGCGCAGAGATGAGCTGAGTGGGGCTTGAAGGTTGTATG 1018
|      |
DB      1241 GTGCTGAGAGACACACATACGCGCGTGCAGTGAATGAGTGGGGCTTGAAGGTTGTATG 1300
|      |
QY      1019 TATGAAATATATGTTGGAGAGTTTACTTTCTACACACAGACCATGAGAACTTTTGA 1078
|      |
DB      1301 TATGAGATGATGTGTGCGCGCTGCGCTTCTACACACAGACCATGAGAGCTGTTGAG 1360
|      |
QY      1079 TTAATTTATGAGACATTTAATTTCTGAAACCTCTTCAATGCAATGCAATGATG 1138
|      |
DB      1361 CTGATCTCATGAGAGATGCGCTTCCGCGACACTGCGCTGAGGCAAGTCTG 1420
|      |
QY      1139 CTTTCAGGCGCTCTGATTAAGATCCAAATPAAACGCTTGTGAGAGACCATGATGATG 1198
|      |
DB      1421 CTCTCGGCGCTGCTCAAGAGACCTTACACAGAGCTGAGTGGGGCTTGAAGATGCG 1480
|      |
QY      1199 AAGAAATTTATGAGACACAGTTTCTCTGAGATTAACCTGCAAGATTTATGATTA 1258
|      |
DB      1481 AAGAGATGATGAGACACAGTTTCTTTCGCAACATGATGAGATGATGATGAGAG 1540
|      |
QY      1259 AAGCTGTACCTCTTTTAACTCAAGTAACTGAGACATGATCTGATTTTGAAT 1318
|      |
DB      1541 AAGCTGAGCCACCTTTCAAGCCCAAGTACCTCTGAGACATGACACAGTATTTGAT 1600
|      |
QY      1319 GAAGATTTTACAGCTGAGCTATTTCAATPAAACACCTGAAATAATGATGAGATGAT 1378
|      |
DB      1601 GAGAGATTTACAGCTGAGCTATTTCAATPAAACACCTGAAATAATGATGAGATGAT 1654
|      |
QY      1379 ATGAGCTGATGAGACATGAGAGGCGCGCATTTCTCAATTTTCTTACTGCAAGT 1438
|      |
DB      1655 ATGAGATGATGAGACATGAGAGGCGCGCATTTCTCAATTTTCTTACTGCAAGT 1714
|      |
QY      1439 GAGCAGATTAAGTC 1453
|      |
DB      1715 GGCACAGCTGAGGC 1729
|      |

RESULT 8
US-10-735-461-20
; Sequence 20, Application US/10735461
; Publication No. US20050014264A1
; GENERAL INFORMATION:
; APPLICANT: CZECH, Michael P.
; APPLICANT: ZHOU, Qionglian
; APPLICANT: JIANG, Zhen
; TITLE OF INVENTION: METHOD OF INTRODUCING siRNA INTO
; TITLE OF INVENTION: ADIPOCYTES
; FILE REFERENCE: UMY-055
; CURRENT APPLICATION NUMBER: US/10/735,461
; CURRENT FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/432427
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2626
; TYPE: DNA

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ORGANISM: Mus musculus
US-10-735-461-20

48.6%; Score 751.4; DB 19; Length 2626;

Query Match
Best Local Similarity 71.8%; Pred. No. 2.3e-190;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

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QY      8 ATCATGAGCGATGTATACCATTTGTGAAGAAGGTTGGGTTCAAGAGAGGAGGAATATATA 67
DB      281 ACCATGAACGAGTGAAGCATTTGTGAAGAGGGCTGGCTGCACAAAGAGGGGAATATATT 340
QY      68 AAAAAGTGAAGGCCAAGATATTCTTTTGAAGAAGATGGCTCATTCATAGATATATA 127
DB      341 AAAACCTGGCGGCGACGCTACTTCTCTCAAGAAAGATGGCACTTTATTTGGCTAAG 400
QY      128 GAGAAACCTCAAGATGTGAT---TTACCTATCCCTCAACACATTTTCAATGGCAAA 184
DB      401 GAACGAGCTCAAGATGTGATGAGAGAGTCCCACTCAACACTTCTCAATGGCAAA 460
QY      185 TGCCAGTTATGAAACAGAACGACCAAGCCAAACACATTTATATCATGATGTCTCAG 244
DB      461 TGCCAGCTGATGAAGCAGAGGGCCAAAGGCCAACCTTTATCATCCGCTGCTGAG 520
QY      245 TGGACTACTGTTATAGAGAAATTTCTATGATGATCTCAAGAGAAAGGAGAGATGG 304
DB      521 TGGACCAAGTATGAGCGCACCTTCCATGTGAAACCGCTGAGGAGCGGAAAGATGG 580
QY      305 ACAGAAAGCTATCCAGGCTGTAGCAGACAGCTGAGAGGCAAGAAAGAGAGATGAT 364
DB      581 GCCACCGCATTCAGCTGTGCGCGATGATGATGATGATGATGATGATGATGATGATGAT 640
QY      365 TGTAGTCCAACTTCAAAATTTATATATATAGAGAGAGAGATGATGATGATGATGAT 424
DB      641 TTCCGATCAGGCTCAACCGATGACACTCAGGGGCTGAAGAGATGATGATGATGATGAT 700
QY      425 CATC---ATAAAGAAAGCAATGATGATTTTGAATTTTGAATTTTGAATTTTGAAT 481
DB      701 AAGCCAGACCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 760
QY      482 ACTTTGGGAAGTTATTTTGTGAGAGAGAGGCAAGGAAATATCATGATGATGAT 541
DB      761 ACTTTGGGAAGTTATTTTGTGAGAGAGAGGCAAGGCGCTACTATCATGATGAT 820
QY      542 ATTCTGAAGAAAGAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
DB      821 ATCTCAAGAAAGAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 880
QY      602 AGAGTATTAAGAAAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
DB      881 CGTGTCTGAGAAAGTCAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 940
QY      662 AAAAGCCGTTGTGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
DB      941 CACGACCCGCTTCTGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1000
QY      722 TCGAGAGAGCGGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
DB      1001 TCTCGAGAGCGGAGTGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1060
QY      782 GCGTTGAGTATCTATCATTTCCGAAAAG---TTGTGTACCGGATGATCAAGTTGAGAG 838
DB      1061 GCCCTGAGTATCTATCATTTCCGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1120
QY      839 CTAATGCTGAGCAAAAGATGAGCAATTAATAATTAAGATTTTGAATTTTGAAGAGAG 898
DB      1121 CTCATGCTGAGCAAAAGATGAGCAATTAATAATTAAGATTTTGAAGAGAGAGAGAGAG 1180
QY      899 ATCAGAGATGAGCAAGATGAGCAATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 958
DB      1181 ATCAGAGATGAGCAAGATGAGCAATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1240
QY      959 GTGTTGAAGATTAATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1018

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DB      1241 GTGCTGAGAGCAACAGCTACGCGCTGACATGAGCTGTGTGGGCGCTGGTCAATG 1300
QY      1019 TATGAATGATGTGTGGAGGTTTACTTTCTAACAACAGAGACATGAGAACTTTTGA 1078
DB      1301 TATGAGATGATGTGTGGCGCTGCTCTTCAACAACAGAGACATGAGAGAGAGAGAG 1360
QY      1079 TTAATATTAATGAGAGATTAATAATTTCTGAAACATCTCTTCAATGATGCAAAATCAT 1138
DB      1361 CTGATCTCATGAGAGAGATCCGCTTCCGAGCAACTCGGCTGAGGCGCAAGTCCCTG 1420
QY      1139 CTTTCAAGGCTCTTATTAAGATGCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
DB      1421 CTCTCGGAGCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1480
QY      1199 AAAAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1258
DB      1481 AAGAGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1540
QY      1259 AAGCTTGAACCTCTTTTAAACCTCAAGTAAATCTGAGAGAGAGAGATATTTGAT 1318
DB      1541 AAGCTGAGCCACCTTTCAAGCCCAAGTCACTCTGAGAGAGAGAGAGAGAGAGAGAG 1600
QY      1319 GAGAAATTTTACAGCTCAAGCTATTTATCAATTAAGAGAGAGAGAGAGAGAGAGAG 1378
DB      1601 GAGAGTTTCAAGCTCAAGATGATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1654
QY      1379 ATGAGCTGATGAGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1438
DB      1655 ATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1714
QY      1439 GGACGAGATTAAGTC 1453
DB      1715 GGACAGAGCTGAGGC 1729

RESULT 9
US-10-895-225A-56
; Sequence 56, Application US/10895225A
; Publication No. US20050048587A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Snyder, Jessica
; APPLICANT: Bagley, Andria
; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
; TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: TLN-025
; CURRENT APPLICATION NUMBER: US/10/895,225A
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/488,502
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 56
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-895-225A-56

Query Match
Best Local Similarity 71.8%; Pred. No. 2.3e-190;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

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185 TGCCAGTATGAAACAGAGCAAGCCAAACATTTATATAGATGTCACG 244
DB 461 TGCCAGTATGAAACAGAGCGGCCAAGCCCAACCTTTATATCCGCTGCACG 520
QY 245 TGGACTACTGTTATAGAGAACTTTCAATGTAGATCTCCAGAGAAAGAGATG 304
DB 521 TGGACCAAGTATATAGAGCACTTCATGTGGAAACGCTGAGAGCGGGAATGG 580
QY 305 ACAGAACTATCCAGGCTGTAGCAGACAGCTGCAAGGCAAGAGAGAGATGAAT 364
DB 581 GCCACCGCATTCAGACTGTGGCCGATGACTCAAGAGGCAAGAAAGAGAGATGAG 640
QY 365 TGTAGTCCAACTTCACAAATGTGTAATATAGAGAGAGAGATGCTCTACAAC 424
DB 641 TTCGATCAGGCTCACCAGTGCAACTCAGGGGCTGAAGAGATGAGGTGCTCGGCC 700
QY 425 CATC--ATPAAAGAAAGCAATGAATGATTTTGAATTTGAATCTAGGTAAAGC 481
DB 701 AAGCCCAAGCACCGTGTGACATGAAAGAGCTTGAATCTGAACTACGCGCAAGGC 760
QY 482 ACTTTTGGAAAGTATTTTGTGTCAGAGAAAGCAAGTGAATAATCTATGCTATGA 541
DB 761 ACTTTTGGAAAGTATTTGTCAGAGAAAGCAAGGCGCTACTATGCTATGAAG 820
QY 542 ATTCTGAAGAAAGAACTCATTTATGCAAGAGATGAGTGGCACAACCTGAATGAAG 601
DB 821 ATCTCAAGAAAGAGTCACTGTCGCAAGAGATGAGTGGCCACACGCTTACTGTGAAC 880
QY 602 AGAGTATTAAGAACTAGACATCCCTTTTAACTCTTGAATAATCTCTCCAGACA 661
DB 881 CGGTCTCTGCAAGACTCTAGGCACTCCCTCTTCAAGGCTCAAGTACTATCCAGACC 940
QY 662 AAAAGCCGTTTGTGTTGTGATGAAATGTTAATGGGGGCGAGCTGTTTTCATTTG 721
DB 941 CAGACCGGCTGCTGTTGTGATGAGTATGCAAGGGGGCGAGCTTCTTCCACCTG 1000
QY 722 TCGAGAGAGCGGCTGTTCTCTGAGACCGCACGCTTTCTATGCTGCAAGAAATGCTCT 781
DB 1001 TCTCGAGAGCGGCTGTTCTCTGAGACCGGGCCCGCTTCTATGCTGCGAGATTTGCTCT 1060
QY 782 GCGTTGAGATCTATCATTTCCGGAAGA--TTGTGACCGTATCTCAAGTTGAGAAAT 838
DB 1061 GCGCTGAGATCTATCTGACATCCAGAAAGAGTGTGTAACGGGACCTGAAAGCTGAGAAC 1120
QY 839 CTAAATCTGCAAAAGATGCGCATPAAATTAACAGATTTTGAATTTGCAAGAGAG 898
DB 1121 CTCATCTGCAAAAGATGCGGCATCAAGATPAAAGACTTGGGCTGTGCAAGAGAGG 1180
QY 899 ATCAAGATGCAAGCCCATGAAAGACATTTCTGTGCACTTCAGAAATCTGAGCAAGAG 958
DB 1181 ATCAAGATGCTGCACTATGAAAGATTTCTGGAACCGCGGAGTACCTGGCCCTGAG 1240
QY 959 GTGTTGAAGATPAAATGATGAGCGAGAGTGAAGTGTGGGGGCTTGAAGGTTGTCTATG 1018
DB 1241 GTGCTGAGAGCAACATGACGCGCTGTGAGTGAATGTGTGGGGGCTGGGCGTGTGATG 1300
QY 1019 TATGAAGATGATGTGGAGAGTTACCTTTCTACACCAAGCAAGCATGAGAAATCTTTTGA 1078
DB 1301 TATGAAGATGATGTGGCGGCTGTGCTTCAACACAGGACCAAGAAAGCTGTTGAG 1360
QY 1079 TTAATTTATGAGAAACATTAATTTCTCTGAAACACTCTCTTCAAGTGAATAATCATG 1138
DB 1361 CTGATCTCATGAGAGATGCGCTTCCGCGCAACTCGGCCCTTGAAGGCAAGTCCCTG 1420
QY 1139 CTTCAGGAGCTCTTGAATAAGATCCAAATPAAAGCCTTGTGAGAGACCAAGATGATGA 1198
DB 1421 CTCTCGGGGCTGTCAAGAAAGACCTTACACAGAGGCTGTGTGGGGCTTGAAGATGCC 1480
QY 1199 AAAAGAAATTAAGACACAGTTTCTTCTGTGAGTAACTGGCAAGATGTATATGATPAA 1258
DB 1481 AAGGAGATCATGACACCGGTTCTTTGCAACATGCTGTGGCAGAGATGTATGAGAG 1540

QY 1259 AAGCTTATGACTCTCTTTTAACTCAAGTATCATGAGACAGATCTAGATTTTGTAT 1318
DB 1541 AAGCTGAGCCCACTTTCAAGCCCAAGTCACTCTGAGACTGACACCGATTTTGTAT 1600
QY 1319 GAAGAAATTTAAGCTCAGACTATTTAATPAAACCACTGAAATAATGATGAGATGAT 1378
DB 1601 GAGGATTCACAGCTCAGATGATTCACATCAACGCGGCTG-----ATCAAGATGACAC 1654
QY 1379 ATGAGCTGATGACATGAGAGGCGGCGGCTTTCCCTCAATTTTCTTCACTGCAAGT 1438
DB 1655 ATGAGATGTGTGACAGTGAAGGCGGCGGCTTCCCAAGTTCCTTCACTGCAAGT 1714
QY 1439 GGACGAGATTAAGTC 1453
DB 1715 GGCACAGCTTGAGGC 1729

RESULT 10
US-10-895-225A-36
; Sequence 36, Application US/10895225A
; Publication No. US20050048587A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Snyder, Jessica
; APPLICANT: Bagley, Andrea
; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
; TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: TLN-025
; CURRENT APPLICATION NUMBER: US/10/895,225A
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/488,502
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 2729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-895-225A-36

Query Match 46.7%; Score 722.4; DB 19; Length 2729;
Best Local Similarity 70.4%; Pred. No. 1.4e-182;
Matches 1027; Conservative 0; Mismatches 416; Indels 15; Gaps 4;

QY 5 GTGATCATGAGGATGTTACATTTGTGAAAGAGTGTGGCTTCAGAAAGGCGAGATAT 64
DB 270 GGCACCATGAGGAGAGTGTGCTATTTGAAAGAGGTTGGCTCACAAAGAGGAGTAC 329
DB 65 ATPAAATCTGAGGCGAAAGATCTTCTTTGAAGACAGATGGCTCATCTAGATAT 124
QY 330 ATCAAGATCTGAGGCGGCGACGCTTCTCTCTCAAGATGATGGCACCTTCAATGGCTAC 389
DB 125 AAAAGAAACCTCAAGATGATGATTTACCTTA---TCCCTCAACAACTTTTCAGTGCA 181
QY 390 AAGAGAGGCGCGCAGAGATGAGCAAGGTGAGGCTCCCTCAACAACTTCTGTGGG 449
DB 182 AATGCGAGTTATGAAAAAGAGAGCAACAAAGCAACATTTATATGAGATGCTC 241
QY 450 CAGTGCAGCTGATGAAAGAGAGGCGGCCCGGCCCAACACTTATCATTCGCTGCCCTG 509
DB 242 CAGTGCAGCTGATGAAAGAGAGGCGGCCCGGCCCAACACTTATCATTCGCTGCCCTG 509
QY 510 CAGTGCAGCTGATGAAAGAGAGGCGGCCCGGCCCAACACTTATCATTCGCTGCCCTG 509
DB 302 TGGAGAAAGTATCCAGGCTGTAGCAGACAGACTGCAAGGCGCAAGAGAGAGAGATG 361
QY 570 TGGAGAACCGCATCCAGCTGTGCTGACGCGCTCAAGAAACAGAGAGAGAGAGATG 629
DB 362 AATTGATGTCAACTTCACAAATTTGATTAATATGAGAGAGAGAGATGATGCTCTTACA 421
QY 630 GACTTCGGGTGCGGCTCACCCAGTGAACAATCAGGGGCTGAAGAGATGAGTGTCCCTG 689
DB 422 ACCCATC--ATPAAAGAAAGCAATGAATGATTTTGAATTTGATTTGAACTACTAGTAA 478

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Db      690 GCCAAGCCCAACACCGCGTGAACATGAAGATTGAGTACCTGAACGCTGCGGCAAG 749
Qy      479 GGCACCTTTGGGAAGTTATTTTGTGTGAGAGAGGCAAGGGAATACTATGTATG 538
Db      750 GGCACCTTTGGGAAGTTATTTTGTGTGAGAGAGGCAAGGCGCTACTTACGCAAG 809
Qy      539 AAGATTCTGAAGAAAGAACTATTTATGCAAGAGTGAAGTGGCACACTCTAACTGA 598
Db      810 AAGATCTCAAGAGAGAACTCATCGTGGCAAGAGAGAGTGGCCACACACTCACCGAG 869
Qy      599 AGCAGATTTAAAGAACTAGACATCCCTTTTAACTCTTGAATATTCCTTCAG 658
Db      870 AACCGGCTCTCAGAACTCCAGGACCCCTTCTCACAGCCCTGAAGTACTTTCAG 929
Qy      659 ACAAAGACGTTTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 718
Db      930 ACCCAGACGCGCTCTGCTTTGTGATGATGATGATGATGATGATGATGATGATGAT 989
Qy      719 TTGTGAGAGAGCGGCTGTCTCTGAGACCGCACAGTTTCTATGATGATGATGATGAT 778
Db      990 CTGTCCCGGAGAGGTGTGTCTTCCAGAGACCGGCGCGCTTCTATGCGCTGAGATTG 1049
Qy      779 TCTGCTTGGACTATCTATCTATCTCGAAGA--TTGTGATCGTGTATCTCAAGTTGAG 835
Db      1050 TCAGCCCTGACTACTCTGACTCGAGAGAAAGTGTGTACTCGGAGCTCAAGCTGAG 1109
Qy      836 AATCTAATGCTGAGCAAAAGATGCGCACATAAAATTAAGATTTTGAATTTGCAAGAA 895
Db      1110 AACCTCATCTGACAAAGAGCGGACATTAAAGATACAGACTCGGCGTGTGCAAGAG 1169
Qy      896 GGGATCACAGATGACGCGCACATGAAGACATCTGTGAGACTCCAGATATCTGGACCA 955
Db      1170 GGGATCAAGAGAGCGGCGCACATGAAGACCTTTTGGGACACACTGAGTACTGGCCCC 1229
Qy      956 GAGGTGTAAGAAATATATATATATATATATATATATATATATATATATATATAT 1015
Db      1230 GAGGTGCTGAGAGACATATATATATATATATATATATATATATATATATATATAT 1289
Qy      1016 AAGTATGAATGATGTGTGAGAGGTTACCTTCTCAACAGAGACCATGAGAACTTTT 1075
Db      1290 AAGTATGAATGATGTGTGAGAGGTTACCTTCTCAACAGAGACCATGAGAACTTTT 1349
Qy      1076 GAATTATATATATATATATATATATATATATATATATATATATATATATATATAT 1135
Db      1350 GAGCTCATCTCATGAGAGAGATCCGCTTCCCGGACGCTTGTGCCAGGCGCAAGTCC 1409
Qy      1136 TTGCTTTCAAGGCTCTTGAATAAGATCCAAATPAAAGCTTGTGTGAGAGCAAGTAT 1195
Db      1410 TTGCTTTCAAGGCTCTTGAATAAGATCCCAAGAGAGGCTTGTGTGAGAGGCTCCGAGGAC 1469
Qy      1196 GAAAAAAGAAATATATATATATATATATATATATATATATATATATATATATATAT 1255
Db      1470 GCAAGAGAAATATATATATATATATATATATATATATATATATATATATATATAT 1529
Qy      1256 AAAAAAGCTTGTATCTCTTTTAACTCAAGTAACTATGAGACAGATCTAGATATTTT 1315
Db      1530 AAGAGCTCAGCCACCTTCAAGCCCAAGTCAAGTCCGAGACATGACACAGATTTT 1589
Qy      1316 GATGAAGATTTTACAGCTCAGACTATTAATTAACACCACTGAAAAATATATATAGAG 1375
Db      1590 GATGAGAGTTTACAGGCTCAGATGATCAACATCAACCACTGACCA-----GATGAC 1643
Qy      1376 GGTATGATGATGAGCAATAGAGAGCGGCGCATTTCCCTCAATTTCTACTCTGAG 1435
Db      1644 AAGATGAGATGTGTGAGACAGAGCGCAAGCGCCCACTTCCCAAGTTCTTACTCGGC 1703
Qy      1436 AGTGAAGAGAAATAGTC 1453
Db      1704 AGCGGACGCGCTGAGGC 1721

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RESULT 11

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US-09-955-999-43
; Sequence 43, Application US/09955999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
; FILE REFERENCE: PTO86P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 2978
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2947)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2973)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-955-999-43

```

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Query Match      46.7%; Score 722.4; DB 10; Length 2978;
Best Local Similarity 70.4%; Pred. No. 1.5e-182;
Matches 1027; Conservative 0; Mismatches 416; Indels 15; Gaps 4;

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Qy      5 GTCATCATGAGCGATGTTATCCATTGTGAAGAAGTTGGCTTCAGAAAGGAGAAATAT 64
Db      485 GGCACCATGAGGAGAGTGTGCTATTTGTGAAGAGGTTGGCTGCACAAAGAGGAGTAC 544
Qy      65 ATAAAAATGAGAGCGCAAGATCTCTTTTGAAGACAGATGGCTCATCTATGATAT 124
Db      545 ATCAAGACTTGGCGGCCACGCTACTTCTCTCAAGAAATGATGACCTTCAATTGGCTAC 604
Qy      125 AAGAGAAACCTCAAGATGTGATTTACCTTA--TCCCTCAACAACTTTTCACTGACA 181
Db      605 AAGAGCGCGCGCAGATGTGAGCAAGTGAAGTGAAGTCCCTCAACAACTTCTGTGGCG 664
Qy      182 AATGCGATTAATGAAAAAGAACAGACCAAGCCAAACACTTTATATATAGATGTCTC 241
Db      665 CAGTCCAGCTGATGAAGACGAGCGGCCCGGCCCAACACTTATCATCGCTGCGCTG 724
Qy      242 CAGTGACATCTGTATATGAGAGAACTTTCATGTATGATCTCGAGAGAAAGGAGAA 301
Db      725 CAGTGACATCTGTATGAGAGCACTTTCATGTGAGATCTCGAGAGCGGAGAGAG 784
Qy      302 TGAAGAGAGCTATCAAGCTGTATGACAGACAGCTGACAGAGCAAGAGAGAGAGATG 361
Db      785 TGAAGACCGCATCAAGATGTGCTGACCGGCTCAAGAGAGAGAGAGAGAGAGATG 844
Qy      362 AATGTAGTCAACTTCAAAATGATATATATATGAGAGAGAGAGAGATGATGCTCTTACA 421
Db      845 GACTTCCGCTCGGCGTCAACCGAGTGAACACTCAGAGGCGTGAAGATGAGAGTGTCCCTG 904
Qy      422 ACCGATC--ATAAAGAAAGCAATGATGATTTTGAATTTGAATCTAAGTAA 478
Db      905 GCAAGCCCAAGACCGGCTGACATGAACGATTTGATGATCTAAGCTGTGGCAGAG 964
Qy      479 GGCACCTTTGGGAAGTTATTTTGTGTGAGAGAGCAAGTGAAGAAATATCTATGATG 538
Db      965 GGCACCTTTGGGAAGTGTATCTGTGTAAGAGAGAGCAAGCGCGCTACTACGCAATG 1024
Qy      539 AAGATTCTGAAGAAAGAGTCTTATTTGCAAGATGATGAGTGAAGTGAAGTGAAGTGA 598
Db      1025 AAGATCTCAAGAGAAAGAGTCTGTGCGCAAGAGAGAGTGGCCCACTACACTCACAG 1084

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QY 599 AGGAGATATTAAAGAACTAGACATCCCTTTTAAACATCTTGAATATCTCCAG 658
DB 1085 AACCGGCTCTGAGAACTCAGGACACCTTCTCAACACCTGAAAGTACTCTTCAG 1144
QY 659 ACAAAAGACCGTTGTTGTTTGTGATGAAATATGTTAATGGGGGCGAGCTGTTTCCAT 718
DB 1145 ACCCAAGACCGCTCTGCTTGTCTGTCTGAGAGTACGCCAAGGGGGGCGAGCTTCTCCAC 1204
QY 719 TTGTGAGAGAGCGGGGTGTTCTGTGAGAGACCGACACGTTTCTATGCTGAGAAATGTC 778
DB 1205 CTGTCCCGGAGGCTGTGTTCTCCGAGAGACCGGGCCCGCTTCTATGGCGCTGAGATTGTC 1264
QY 779 TCTGCTTGAATCTATCTACATTCGGAAAGA---TTGTGATCCGTATCTCAAGTTGAG 835
DB 1265 TCAGCCCTGAGACTGACCTGAGAGAAAGACGTGTGTGACCGGACCTCAAGCTGAGAG 1324
QY 836 AATCTAATGCTGAGCAAAAGATGCGCACATATAAATTAACAGATTTTGAATTTGCAAAAGA 895
DB 1325 AACTCATGCTGAGCAAGAGACGGGACATTAAGATCAGACTTCGGGCTGTCCAGAG 1384
QY 896 GGGATCAAGAGTCAAGACCATGAGAGACATCTGTGAGACCTCAAGATATCTGGACCA 955
DB 1385 GGGATCAAGAGCGGTGCGACCATGAGAGACCTTTTGGCGGACACTGAGTACTGGCCCC 1444
QY 956 GAGGTGTGAAGATTAATGATCTATGGCCGAGAGTACCTGTGTGGGCTTGAAGGCTTGTG 1015
DB 1445 GAGGTGTGAAGACATGATCTACGGCCGAGAGTACCTGTGTGGGCTTGAAGGCTTGTG 1504
QY 1016 ATGTATGAATATGATGTGTGAGAGTTACCTTTTCAACACAGAGACCATGAAATCTTTT 1075
DB 1505 ATGTATGAAGATGATGTGTGAGAGTTACCTTTTCAACACAGAGACCATGAAATCTTTT 1564
QY 1076 GAATTAATATTAATGAGACATTAATTTCTGAAACACTCTTCTGAGTGAATAATCA 1135
DB 1565 GAGCTCATCTCATGAGAGAGATCCGCTTCCCGGACAGCTTGTGCTCCGAGGCAAGTCC 1624
QY 1136 TTGCTTTCAGGCTCTTGAATTAAGATCCAAATTAAGCGCTTGTGTGAGAGACAGATGAT 1195
DB 1625 TTGCTTTCAGGCTCTTGAATTAAGATCCAAATTAAGCGCTTGTGTGAGAGACAGATGAT 1684
QY 1196 GCATAAAGAAATTAATGAGACACAGATTTCTCTGAGATTAATCTGCAAGATGATATGAT 1255
DB 1685 GCCAAGAGATCTATGACGATCTGCTTCTTCCGGATGATGTGTGAGAGACAGTGTACAG 1744
QY 1256 AAAAAGCTGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATTAATATTTT 1315
DB 1745 AAGAAGCTGAGCCACCTTCAAGCCCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1804
QY 1316 GATGAAGATTTTACAGTCTGAGATTAATTAACACCACTGAAATTAATGATGAGAT 1375
DB 1805 GATGAAGATTTTACAGGCTGAGATTAATTAACACCACTGAAATTAATGATGAGAT 1858
QY 1376 GGTATGAGCTGAGTGAAGCAATGAGAGCGGCGGATTTCCCTCAATTTTCTACTCTGCA 1435
DB 1859 AGCATGAGTGTGTGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1918
QY 1436 AGTGAAGAGAAATTAATGAT 1453
DB 1919 AGCGGACAGGCGCTGAGGC 1936

RESULT 12
US-10-072-036-138
; Sequence 138, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: OLE THASTRUP
; APPLICANT: SARA BURON
; APPLICANT: SOREN TULLIN
; APPLICANT: KASPER ALMHOLT
; APPLICANT: KURT SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
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; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072, 036
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/417, 197
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PXB fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-10-072-036-138

Query Match 46.6%; Score 721.2; DB 14; Length 2184;
Best Local Similarity 70.7%; Pred. No. 2.6e-182;
Matches 1021; Conservative 0; Mismatches 408; Indels 15; Gaps 4;

QY 3 GAGTCATCATGAGCCATGTTACATTTGAAAGAGTTGGGTTCAAGAGGAGAGAT 62
DB 734 GAGGACCATGAGCCATGAGGCTGATTTGTGAAGAGGTTGGCTGCACAAACAGAGGAGT 793
QY 63 ATATATAAACTGAGAGCCAGATATCTTTTGAAGACAGATGCTCATTAATAGAT 122
DB 794 ACATCAAGACCTGAGCGGACCATCTTCTCTCAAGATATGAGCATTTCAATGGCT 853
QY 123 ATTAAGAGAACTCAAGATGTGATTTACTTA---TCCCTCAACAACTTTCAAGTGG 179
DB 854 ACAAGAGAGGCGCGAGATGTGAGCAACGTGAGGCTCCCTCAACAACTTCTGTGG 913
QY 180 CAAATGCGAGTTAATGAAGAAAGAGAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 239
DB 914 CGGAGTCCAGCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 973
QY 240 TCCAGTGAATCTATGTTATGAGAGAACTTCTGATGATATCTTCAAGAGAAAGGAGAG 299
DB 974 TGAAGTGAAGCACTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1033
QY 300 AATGAGCAAGATCTATCCAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
DB 1034 AGTGAAGCAAGCCGATCCAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1093
QY 360 TGAATGTGATCAACTTCAAGAAATGATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 1094 TGAATGTGATCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1153
QY 420 CAAGCCATC---ATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
DB 1154 TGGCCAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1213
QY 477 AAGGCACTTTTGGAGAAATTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
DB 1214 AAGGCACTTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1273
QY 537 TGAAGATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 596
DB 1274 TGAAGATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1333
QY 597 AAGCAGAGATTAATGAAGCACTAGACATCCCTTTTAAACATCTTGAATATTCCTTCC 656
DB 1334 AAGACCGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1393
QY 657 AAGCAAAAGACCGTTGTTGTTTGTGATGAGATATGTTAATGGGGGCGAGCTGTTTTC 716
DB 1394 AAGCCAGAGAGCGGCTGCTTGTCTGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1453
QY 717 ATTGTGAGAGAGAGGAGTGTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 776
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1454 ACCGTCCCGGGAACGTGTCTTCGAGACCGGCGCTTCTATGCGCTGAGATTG 1513
777 TCTCTGCTTGGAGCTATCTACATTCGGAAGA--TTGTGATACGCTGATCTCAAGTTGG 833
1514 TGTCAAGCTTGGATCTCTGCACTCGGAGAGAGACCTGATGACCGGAGCTTCAAGCTGG 1573
834 AGAATTAATGCTGACAAAGATGCGCACATTAATAATTAACAATTTGGACTTTGGCAAG 893
1574 ACAAACCTGCTGACAAAGACCGGCAATTAAGATCAACAAGCTTCCGGCTGTGCAAG 1633
894 AAGGATCAAGATGACGACCACTAATAAGACATTTCTGTGGCACTCCAGATATCTGGCAC 953
1634 AAGGATCAAGACCGGTGCGACCATTAACCTTTTGGCGACACTGTGATCTGGCCCC 1693
954 CAGAGCTGTTAAGATTAATGACTATGCGCGAGCACTAGTGTGGGCGCTAGGGGTTG 1013
1694 CCGAGGTGCTGAGAGCAATGACTACGCGCTGCACTGATGATGATGATGATGATGATG 1753
1014 TCATGTATGAAAATGATGTGTGGAGGTTACCTTTTCAACAGACAGACATGAGAACTTT 1073
1754 TCATGTACGAGATGATGTGCGGTGCGCTGCTTCTTACAAACAGACAGACATGAGAACTTT 1813
1074 TTGAATTAATTAATGAGAGACATTAATTTCTGTGAACTCTTCTTCAATGCAAAAT 1133
1814 TTGAGCTCATCTCTCAAGAGAGATCCGCTTCCCGGCAAGCTTGTGCTCCGAGGCCAAGT 1873
1134 CATGCTTCAAGGCTCTTGTATTAAGATTCAAATTAAGCGCTTGGTGGAGACAGATG 1193
1874 CTTGCTTCAAGGCTGCTCAAGAGAGACCCCAAGAGAGGCTTGGCGGGGCTCCGAGG 1933
1194 ATGCAAAAGAAATTAAGACACAGTTTCTTCTGTGAGTAACTGGCAAGATGATATG 1253
1934 ACGCCAAAGAGATCATGAGACATGCTTCTTGGCGGTATGATGATGAGACAGTATAG 1993
1254 ATAAAAAGTTGACTCTCTTTTAACTCAAGTAACTGTGAGACAGATTAAGTATTT 1313
1994 AAGAGAGCTCAGCCCACTTCAAGCCAGGTACAGTGAAGATGACACCAAGATAT 2053
1314 TTGATGAAGAAATTAAGCTCAGACTATTAACAATAACCACTGAAAAATATGATGAG 1373
2054 TTGATGAGAGATTCACGCGCCAGATATCACTACACCACTGACCA-----GATG 2107
1374 ATGATGAGCTGATGACAAATGAGAGCGCGCGCATTTCCCTCAATTTCTTACTCTG 1433
2108 ACAGATGAGATGTGTGACAGCAGGAGCGAGCGCCCACTTCCCGCACTTCTCTACTCG 2167
1434 CAAAG 1437
2168 CCAAG 2171

Db

RESULT 13
US-09-970-000-3
Sequence 3, Application US/0970000
Patent No. US20020127214A1
GENERAL INFORMATION:
Applicant: Hemmings, Brian Arthur
Title of Invention: Rac-Protein Kinase as Therapeutic Agent
Or In Diagnostics
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020127214A1atlis Patent and Trademark Department
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/970,000
FILING DATE: 03-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/068,702
FILING DATE: 13-May-1998
APPLICATION NUMBER: PCT/EP96/04810
FILING DATE: 11-May-1996
APPLICATION NUMBER: GB 9523379, 7
FILING DATE: 16-No. US20020127214A1-1995
APPLICATION NUMBER: GB 9525704, 4
FILING DATE: 15-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Diane E.
REGISTRATION NUMBER: 31,104
REFERENCE/DOCKET NUMBER: 4-20635/A/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6924
TELEFAX: (908) 522-6955
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Human RAC alpha
FEATURE:
NAME/KEY: CDS
LOCATION: 199..1641
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 199..1641
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-970-000-3

Query Match 46.5%; Score 719.2; DB 9; Length 2610;
Best Local Similarity 70.3%; Pred. No. 1e-181;
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

Db

5 GTCAATCAGAGGAGATTAACATTTGAAAGAGGTTGGGTTCAAGAGGAGGAGATAT 64
193 GGCACATAGAGGAGATGCTATTTGTGAAGAGGTTGGCTGCAAAAGAGGAGATG 252
65 ATAAAACTGAGGCAAGATCTCTTTTGAAGACAGATGCTCATTTCAATGATAT 124
253 ATCAAGACTGCGCGCAAGCTACTTCTCTCAAGATGATGCACTTCAATGGCTAC 312
125 AAAAGAACTCAAGATGTGATTTACCTTA--TCCCTCAACAATTTCAATGGCA 181
313 AAGAGCGCGCGCAGATGTGACCAAGGTGAGGCTCCCTCAACAATTTCTGTGGCG 372
182 AAATCCGATTAATGAACAGACGACCAAGCCAAACACATTTATATAGATGTCTC 241
373 CAGTCCAGCTATTAAGAGAGAGGCGCGCCGCGCCCAACCTTATCATTCGCTGCTG 432
242 CAGTGAATCTGTTATAGAGAACTTTCAATGATGATCTCCAGAGAGAAAGAGAGAA 301
433 CAGTGAACACTGTATGAGAGCAGCTTCCATGTGAGAGCTCCTGAGAGAGGAGAG 492
493 TGAACAACCGCCATCAAGCTGTGCTGACGCGCTCAAGAGAGAGAGAGAGAGATG 552
302 TGAACAAGAGCTATTCAGGCTGTAGAGACAGACTGCAAGGCAAGAGAGAGAGATG 361
436 AATGTATGCAACTTCAATTAATTAATTAAGAGAGAGAGAGAGAGATGCTCTACA 421
553 GACTTCGGTGGGCTCAGCCAGTGAACAATTCAGAGGCTGAAGAGATGAGATGCTCCTG 612
422 ACCCATC--ATAAAGAAAGCAATGATGATTTTGAATATTTGAATTAAGTAA 478


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Db 613 GCCAAGCCCAAGACCCGCGACCATGAGAGTTTAACTGGAAGCTGCGGGAG 672
Qy 479 GGCACCTTTGGGAAAGTATTTGGTTCGAGAGAGCAAGTGAATAATCTATGCTATG 538
Db 673 GGGACCTTTGGGCAAGGATCTGGTGAAGAGAGGCAAGGCCCTACTAGCCATG 732
Qy 539 AAGATTCGAAAGAAAGATCATTTATGCAAGAGTGAAGTGGACACCTTAAGCTGA 598
Db 733 AAGATCTCAAGAGAGATGATCTGGCCAGAGAGAGTGGCCACACATCTACCCAG 792
Qy 599 AGCAGATATTAAAGAACATAGACATCCCTTTTAAATCTCTTGAATATTTCTTCAG 658
Db 793 AACGGCTCTCGAGAGACTCGAGGACCCCTTCTCAGACCCCTGAAGTACTCTTCAG 852
Qy 659 ACAAAGACCGTTGTGTTGTTGATGGAATATGTTATGGGGGCGAGCTGTTTCAT 718
Db 853 ACCACACACCGCTCTGCTTGTTCATGAGTACGCCAACGGGGCGAGCTGTTCTCAC 912
Qy 719 TTGTCGAGAGAGGGGTTCTCTGAGAGACCGCACAGTTTCTATGGTGAAGAAATGTC 778
Db 913 CTGTCCCGGAGACGTGTTCTCGAGAGACCGGGCCGCTTCTATGGCGCTGAGATTGTC 972
Qy 779 TCTGCCCTTGGACTATCTACATTCGGAAGAA--TTGTATACCGTGATCTCAAGTTGGAG 835
Db 973 TCAGCCCTGGACTACTGCACTCGAGAGAGACGTGTTATCCGGGACTCAAGCTGGAG 1032
Qy 836 AATCTAATGCTGCAAAAGATGCCACATAAATTAACAGATTTGACTTTGCAAGAA 895
Db 1033 AACCTCATGCTGGCAAGAGACGGGCATTAAGATCAACAGCTTCGGGGCTGTGCAAGAG 1092
Qy 896 GGGATCACAATGACGACCAATGAAGACATTCGTGGCACTCCAGAAATCTTGGGCCA 955
Db 1093 GGGATCAGAAGACGTGTCACCAATGAAGACCTTTTGGCGCACCTGTGATCTGGGCCCC 1152
Qy 956 GAGGTGTTAAGATTAATGACTATGCGCGAGAGTACGTGTGGGCTTGAAGGGTGTGC 1015
Db 1153 GAGGTGTGAGAGCAATGACTAGCGCGGTGAGTGAATGTGTGGGGCTGTGGGTGTGC 1212
Qy 1016 ATGTATGAATGATGTGTGGAGGTTACTTTTCAACAACAAGACATGAGAACTTTT 1075
Db 1213 ATGTACAGATGATGTGTGGGTGCGCTTCCCTTCAACAACAAGACATGAGAACTTTT 1272
Qy 1076 GAATTAATATTATGAGACATTAATTTCTCGAACACTCTCTTCAAGTGAATAATCA 1135
Db 1273 GAGCTATCTCAATGAGAGATCCGCTTCCGCGACGCTTGTGCGAGGCCAAGTCC 1332
Qy 1136 TTGCTTTCAAGGCTCTTGATTAAGATCAAAATTAACGCTTGGTGAAGACAGATGAT 1195
Db 1333 TTGCTTTCAAGGCTCTCAAGAAAGACCCCAAGAGAGCTTGGCGGGGCTCCGAGAC 1392
Qy 1196 GCAAAAGAAATTAAGACACAGTTTCTTCTGAGATTAACCTGGCAAGATGATATGAT 1255
Db 1393 GCCAAGAGATCATGACGATCGCTTCTTGGCGGTATCGTGTGGACAGCATGTAGAG 1452
Qy 1256 AAAAGCTTGTACTCTTTTAAACCTCAAGTAACTCTGAGACAGTACTAATATTTT 1315
Db 1453 AAGAGCTCAAGCCACCTTCAAGCCCAAGTCAAGTGAAGTGAACAGATATTTT 1512
Qy 1316 GATGAAGATTTACAGCTCAGACTATTAACAATAACCACTGAAAAATATGATGAGAT 1375
Db 1513 GATGAAGATTTCAAGCCCAAGTGAATCAATCAACCACTGACCA-----GATGAC 1566
Qy 1376 GGTATGAGCTGCAATGCAATGAGAGGCGCGCATTTCCCTCAATTTCTTACTGCA 1435
Db 1567 AGCATGAGATGTGTGACAGAGCGAGCGACCTTCCCAAGTTCTCTACTGCGGC 1526
Qy 1436 AGTGAAGAGAAATGATC 1453
Db 1627 AGCAGCAGGCGCTGAGGC 1644
```

RESULT 14

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US-10-388-263-329
; Sequence 329, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Onishi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199) ... (1641)
US-10-388-263-329
```

Query Match 46.5%; Score 719.2; DB 17; Length 2610;
Best Local Similarity 70.3%; Pred. No. 1e-181;
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

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Qy 5 GTCATCATGAGCGCATGTTACATTTGGAAGAGTGTGGTTGCAAGAGGGGAGATAT 64
Db 193 GGCACATGAGCAGCAGCTGCTATTTGAAAGAGGTTGGCTGCAAAAGAGGAGTAC 252
Qy 65 ATAAAAAATGAGGCGCAAGATATCTCTTTGGAAGACAGATGGCTCATTTAGATAT 124
Db 253 ATCAAGACCTGGGGGCGCAAGCTACTTCTCTCAAGAAATGATGGCACCTTCAATGGCTAC 312
Qy 125 AAGAGAAACCTCAAGATGTGATTTACCTTA---TCCCTGAACAACCTTTTCAAGTGGCA 181
Db 313 AAGAGACCGCGGAGATGTGACCAAGCTGAGGCTCCCTCAACAACCTTCTGTGGCG 372
Qy 182 AATGCGAGTTATGAAAAAGAAAGACCAAGCAACATTTATTAATCAATGATCTC 241
Db 373 CAGTGCAGCTGATGAAAGACGAGCGGCCGCCCAACACCTTCAATCGCTGCTG 432
Qy 242 CAGTGAATGATGTTATGAGAAACATTTCAATGATATCTCAGAGAAAGGAGAA 301
Db 433 CAGTGAACCACTGATGAAAGACGAGCGGCCGCCCAACACCTTCAATCGCTGCTG 492
Qy 302 TGAAGCAAGCTATCAAGCTGTAGACAGACTCCAGAGGCAAGAGAGAGAGATG 351
Db 493 TGAACCAAGCAATCAAGACTGTGCTGACGCGCTCAAGAAAGAGAGAGAGATG 552
Qy 362 AATGTAGTCAACTTCAACAAATTAATATATATGAGAGAGAGATGATGCTCTAC 421
Db 553 GATTTCCGGTGGGCTCACCACATGCAACTCAAGGGCTGAAAGATGAGTGTCTCG 612
Qy 422 ACCCATC---ATTAAGAAAGACAAATGAATGATTTTGAATTTGAATCACTAGTAA 478
Db 613 GCCAAGCCCAAGACCGCGTGAACATGAGAGAGTTTGAATGATGAGTGTGCTGGCAAG 672
Qy 479 GGCACCTTTGGGAAAGTATTTTGGTTGCAAGAGGCAAGTGAATAATCTATGCTATG 538
Db 673 GGCACCTTTGGGAAAGTGTATCTGTGGAAGAGAGGCAAGGCGCTTACTACGCAATG 732
Qy 539 AAGATCTGAAGAAAGATGATTTATTTGCAAAAGATGAAGTGGACACACTTAAGTGA 598
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Dh 613 GCCAAGCCCAAGCAGCGGTGACCATGAACGAGTTTGATGTAACCTGAAGCTGTGGCAAG 672
Qy 479 GGCACCTTTGGGAAAGTATTTGGTTCGAGAGAGCAAGTGGAAATATCTATGCTATG 538
Dh 673 GGCACCTTTGGGAAAGTATTTGGTTCGAGAGAGCAAGTGGAAATATCTATGCTATG 732
Qy 539 AAGATCTGAAAGAAAGATCATTTATGCAAGAGATGAAGTGGACACACTTAACGTAA 598
Dh 733 AAGATCTCAAGAGAGATCATTTGCGCCAAAGAGAGAGTGGCCACACACTCAACGAG 792
Qy 599 AGCAGAGTATTAAGAACACTAGACATCCCTTTTAAACATCTTGAATATTCCTTCAG 658
Dh 793 AACCGGCTCTGCAAGATCTCAAGCAACCTTCCTCAAGCCCTGAAGTACTCTTCAG 852
Qy 659 ACAAAGACCGCTTGTGTTTGTGATGGAATATGTAATGAGGCGAGCTGTTTTCAT 718
Dh 853 ACCCAAGACCGCTCTGCTTGTGATGGAATATGTAATGAGGCGAGCTGTTTTCAT 912
Qy 719 TTGTCGAGAGAGCGGGTGTCTGAGGACCGCAAGTTTCTATGATGCAAAATTTGTC 778
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CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsgood, H.,
 Kowitz, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
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 Series: IRAK Plate: 13 Row: h Column: 23
 This clone was selected for full length sequencing because it
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 VERSION AY399351.1 GI:39755340
 KEYWORDS GSS.

ORGANISM

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 1 (bases 1 to 1440)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,

REFERENCE

AUTHORS

TITLE Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1440)
AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Substition
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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genomic survey sequence.
ACCESSION AY399353
VERSION AY399353.1 GI:39755342
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielsen,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302
 2 (bases 1 to 1394)
 REFERENCE
 AUTHORS
 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C.,
 Adams,M.D. and Cargill,M.
 TITLE
 JOURNAL
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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 genomic survey sequence.
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 VERSION
 AY399352.1 GI:39755341
 KEYWORDS
 GSS.
 SOURCE
 Pan troglodytes (chimpanzee)
 ORGANISM
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 REFERENCE
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 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C.,
 Adams,M.D. and Cargill,M.
 TITLE
 JOURNAL
 Science 302 (5652), 1960-1963 (2003)
 PUBMED
 14671302
 2 (bases 1 to 1440)
 REFERENCE
 AUTHORS
 Clark,A.G., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
 Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,

Peritiera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adam, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Location/Qualifiers

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Best Local Similarity 70.0%; Pred. No. 6,6e-252;
Matches 1008; Conservative 0; Mismatches 432; Indels 0; Gaps 0;

QY 11 ATGAGCGATGTTACCATTTGAAAGAAAGTTGGGTTTCAAGAGGGGAGAAATATATAAA 70
DB 1 ATGAGCGATGTTACCATTTGAAAGAAAGTTGGGTTTCAAGAGGGGAGAAATATATAAA 60
QY 71 AACTGAGGCGCAAGATCTCTTTTGAAGACAGATGGCTCATTCATAGATATATAAG 130
DB 61 AACTGAGGCGCAAGATCTCTTTTGAAGACAGATGGCTCATTCATAGATATATAAG 120
QY 131 AAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCGAG 190
DB 121 AAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCGAG 180
QY 191 TTAATGAAAACAGACGACCAAAAGCCAAACATTTAATCATGATGTCTCCAGTGACT 250
DB 181 TTAATGAAAACAGACGACCAAAAGCCAAACATTTAATCATGATGTCTCCAGTGACT 240
QY 251 ACTGTTATAGAGAACTTCTATGATATCTCCAGAGAAAGGAAATGACAGAA 310
DB 241 ACTGTTATAGAGAACTTCTATGATATCTCCAGAGAAAGGAAATGACAGAA 300
QY 311 GCTATCAGGCTGTAGACAGACTGACAGAGGCAAGAAAGAGAGATGATTTAGT 370
DB 301 GCTATCAGGCTGTAGACAGACTGACAGAGGCAAGAAAGAGAGATGATTTAGT 360
QY 371 CCAACTTCACAAATGTGATAATATAGAGAGAAAGATGATGCTCTACACCATCAT 430
DB 361 CCAACTTCACAAATGTGATAATATAGAGAGAAAGATGATGCTCTACACCATCAT 420
QY 431 AAAAGAAAGCATGATGATTTTGAATATTTGAACTACTAGATAAGCACTTTTGGG 490
DB 421 AAAAGAAAGCATGATGATTTTGAATATTTGAACTACTAGATAAGCACTTTTGGG 480
QY 491 AAAGTATTTTGGTTCAGAGAGGCAAGTGAATAATATATATGAAATTTGAG 550
DB 481 AAAGTATTTTGGTTCAGAGAGGCAAGTGAATAATATATGAAATTTGAG 540
QY 551 AAAAGATCATTTATGCAAGATGAAAGTGGCAACACTTAACTGAAGCAGATATTA 610
DB 541 AAAAGATCATTTATGCAAGATGAAAGTGGCAACACTTAACTGAAGCAGATATTA 600
QY 611 AAGAACATGACATCCCTTTTAACTCTTGAATAATCTCTCCAGACAAAAGCCGT 670
DB 601 AAGAACATGACATCCCTTTTAACTCTTGAATAATCTCTCCAGACAAAAGCCGT 660
QY 671 TTGTGTTTGTGATGAAATGTTAATGGGGGAGGCTGTTTTTCCATTTTGAAGAG 730
DB 661 TTGTGTTTGTGATGAAATGTTAATGGGGGAGGCTGTTTTTCCATTTTGAAGAG 720
QY 731 CGGGTGTCTCTGAGAGACGCGACACGTTTCTATGATGTCAGAAATGTCTCTGAC 790
DB 721 NNN 780

QY 791 TATCTACATTCGGAAGAAGTGTGTACCGTGATCTCAAGTTGGAGAAATCAATGCTGAC 850
DB 781 NNN 840
QY 851 AAAGATGCGCACATTAATAATTAAGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 910
DB 841 AAAGATGCGCACATTAATAATTAAGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 900
QY 911 GCCACATTAAGACATTTCTGTGGCACTCCAGATATCTGCGACACAGAGGTGTAAGAAT 970
DB 901 NNN 960
QY 971 AATGACTATGCGCGACAGTATGACTGTGTGGGCTGAGGGTTGTATGTAATGATG 1030
DB 961 NNN 1020
QY 1031 TGTGGAGGTTACCTTTCTACACACAGACATGAGAAACTTTTGAATTAATATATG 1090
DB 1021 NNN 1080
QY 1091 GAAGACATTAATTTCTCTGAAACACTCTCTTCAATGCAAAATCATTTCTTCAAGGCTC 1150
DB 1081 GAAGACATTAATTTCTCTGAAACACTCTCTTCAATGCAAAATCATTTCTTCAAGGCTC 1140
QY 1151 TTGATTAAGATTCACAAATAAGGCTTGTGGAGACAGATGATGCAAAAGAAATATG 1210
DB 1141 NGATTAAGATTCACAAATAAGGCTTGTGGAGACAGATGATGCAAAAGAAATATG 1200
QY 1211 AGACACATTTCTCTCTGAGATTAACCTGCAAGATGATATGATATAAGCTTGTACT 1270
DB 1201 NNN 1260
QY 1271 CCTTTAAACCTCAAGTAACTGAGACAGATCTAGATATTTGATGAAGATTTAA 1330
DB 1261 CCTTTAAACCTCAAGTAACTGAGACAGATCTAGATATTTGATGAAGATTTAA 1320
QY 1331 GCTCAGACTTATTAACATACACCTGAAATATGAGAGATGATGATGATGCTGATG 1390
DB 1321 GCTCAGACTTATTAACATACACCTGAAATATGAGAGATGATGATGATGCTGATG 1380
QY 1391 GACATGAGAGGCGGCGGATTTTCTCTCAATTTTCTTCACTGCAAGTGAAGAAATTA 1450
DB 1381 GACATGAGAGGCGGCGGATTTTCTCTCAATTTTCTTCACTGCAAGTGAAGAAATTA 1440

RESULT 5
BUS20318
LOCUS
DEFINITION
AGENCOURT 10157385 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6518260 5', mRNA sequence.
VERSION
BUS20318
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
NIH-MGC <http://mgi.nci.nih.gov/>.
1 (bases 1 to 967)
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM1409 row: 1 column: 05
High quality sequence start: 16
High quality sequence stop: 729.

Oy	263	GAACATTTCACTGTGATACCTCACAAGAAAGAAAGATGACAGAAAGCTATCCAGGCT	322
Db	61	AGAACATTTCACTGTGATACCTCACAAGAAAGAAAGTGGACGAAAGCTATCCAGGC	120
Oy	323	GTAGCAGACAGACTGCAGAGCGCAAGAGAGAGAGATGAATTGTATGTCCACTTCACAA	382
Db	121	GTAGCCGACCGATTTGCAGAGCGCAAGAGAGAGATGAATTGTATGCCCAACTCAGC	180
Oy	383	ATTGATTAATTAGGAGAGAGAGATGGATGCTCTTACCAACCCTATCTAAAGAAAGACA	442
Db	181	ATTGATTAATTAGGAGAGAGAGATGGATGCTCTTACCAACCCTATCTAAAGAAAGACG	240
Oy	443	ATGATGATTTTGACTAATTTGAAACTACAGGTAAAGCACTTTGGGAAAGTTATTTTG	502
Db	241	ATGATGATTTTGACTAATTTGAAACTACAGGTAAAGCACTTTGGGAAAGTTATTTTG	300
Oy	503	GTTCCAGAGAAAGCGCAAGTGGAAAATACTATGCTATGAAGATTCGAAAGAAAGATCAAT	562
Db	301	GTTCCAGAGAAAGCGCAAGTGGAAAATACTATGCTATGAAGATTCGAAAGAAAGATCAAT	360
Oy	563	ATTGCAAAAGATGAAGTGGCACACACTCTAATCTGAAAGCAGATATTAAAGAACCTAGA	622
Db	361	ATTGCAAAAGATGAAGTGGCACACACTCTTACTGAAGCAGATCTAAGAAACACAGAA	420
Oy	623	CATCCCTTTTAAACATCCTGTGAAATATTCCTCCAGACAAAGACCGTTTGCTTTGG	682
Db	421	CATCCCTTTTAAACATCCTGTGAAATATTCCTCCAGACAAAGACCGTTTGCTTTGG	480
Oy	683	ATGGAATATGTTAATAGGGGGCAGAGCTGTTTCCATTTGTCGAGAGAGCGGTGTTCT	742
Db	481	ATGGAATATGTTAATAGGGGGAGAGCTGTTTCCATTTGTCGAGAGAGAGATGTTCT	540
Oy	743	GAGGACCGCACACGTTTCTATGTGTGAGAAATTGCTCTGCTTGCACTATCTACATTC	802
Db	541	GAGGACCGCACACGTTTCTATGTGTGAGAAATTGCTCTGCTTGCACTATCTACATTC	600
Oy	803	GGAAAGATTTGTGTACCGTATCTCAAGTTGGGAATCTAATGCTGGACAAAGATGGCCAC	862
Db	601	GGAAAGATTTGTGTACCGTATCTCAAGTTGGGAATTTGATGCTGATTAAGATGGCAAT	660
Oy	863	ATAAAAATTACAGATTTTGACTTTTGCAAGAAAGAGGATCACAGATGCAGCCACATGAG	922
Db	661	ATTAATAATTACGATTTTGGGCTTTGCANNAAGAGGATCACAGATGCAGCTACATGAG	720
Oy	923	ACATTTCTGTGCACTTCAGAAATATCTGGCACAGAGGTTTGAAGATATGACTATGGC	982
Db	721	ACATTTCTGTGCAACACAGAGTACCTGGCACAGAGGTTTGAAGATATGACTATGGC	780
Oy	983	CGAGCAGTGAATGGTGGGGCCTTAGGGGTTGTCATGTAG	1022
Db	781	CGAGCGTGACTGTGTGGGCTTAAAGTGTGTGATGTATG	820

RESULT	7
CNS27185	
LOCUS	
DEFINITION	CNS27185 798 bp mRNA linear EST 29-APR-2006
ACCESSION	U1-N-HB0-cpc-c-10-0-U1.r1 NIH_BMAP_HB0 Mus musculus cDNA clone IMAGE:30653145 5' , mRNA sequence.
VERSION	CNS27185
KEYWORDS	CNS27185.1 GI:46855341
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL	1 (bases 1 to 798)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1998) Contact: Robert Strauberg, Ph.D. Email: cgapdb-r@mail.nih.gov Tissue Procurement: Dr. James Lin University of Iowa

CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.htm>
This clone was contributed by The Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5
Location/Qualifiers
798

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1: 798
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:3053145"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP HB0"
/notes="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I, The library was constructed according
Bonaldo, Lemmon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TATTGAGT. This library was created for the University of
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

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ORIGIN

Query Match	46.8%;	Score 724;	DB 7;	Length 798;
Best Local Similarity	94.1%;	Pred. No. 4.2e-178;		
Matches 751; Conservative	0;	Mismatches 47;	Indels 0;	Gaps 0

Oy	163	CAACAACCTTTCCAGTGGCAAAATGCGACGTTAATGAAAAACAAGACCAAGCCAAACAC	222
Db	1	CAACAACCTTCCAGTGGCAAAATGCTCAGTTAATGAAAAACAAGACCAAAAGCCAAATAC	60
Oy	223	ATTATTAATCAGATGCTCTCCAGTGGCACTACTGTATAGAGAAACATTTCACTAGATAC	282
Db	61	ATTATTAATCAGATGCTCTCAGTGGACCACTGTATAGAGAAACATTTCACTAGATAC	120
Oy	283	TCCAGAGAAAAGGAAGATGGACGAAGCTATTCAGGCTTAGCACACAGCTGCAGAG	342
Db	121	ACCAGAGGAAAGGAAGATGGACCGAAGCTATCCAGCCCGACCGCATTTGCAGAG	180
Oy	343	GCAAGAAAGGAGAGAAATGTAATTGTATGTCGAACCTTCAAAATTGATAATAGAGAGGA	402
Db	181	GCAAGAGAGAGAGAGATTAATTTGATGCCCACTCAGCATTTGATATATAGAGAAAGA	240
Oy	403	AGAGATGATGCTCTACCAACCATCATPAAAAGAAAGCAATGATGATTTTGACTATT	462
Db	241	AGAGATGATGCTGTACCAACCATCATPAAAAGAAAGCAATGATGATTTTGACTATT	300
Oy	463	GAAACTAATAGTAAAGGCACTTTTGGGAAAGTTATTTGGTTGAGAGAAAGGCAATGG	522
Db	301	GAAACTAATAGTAAAGGCACTTTTGGGAAAGTTATTTGGTTGAGAGAAAGGCAATGG	360
Oy	523	AAAATCTATGCTATGAAGAATCTGAAGAAAGAGTCAATTTCCAAAGATGAAGTGGC	582
Db	361	AAAATCTATGCTATGAAGATTTCTGAAGAAAGAGTCAATTTCCAAAGATGAAGTGGC	420
Oy	583	ACACACTTAATGTAAGAGCAGAGTATTAAAGAACCTAGACATCCCTTTTAACATCTT	642
Db	421	ACACACTTTAATGTAAGAGCAGAGTCTAAAGAACCAAGACATCTATTTTAACATCTT	480
Oy	643	GAAATATCTCTCCAGCAAAAGACCGTTTGTGTTTGTATGGAATATGTTAATGGGGG	702

QY 1079 TTAATATTAAGAGACATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTG 1138
 DB 1254 CTGATCTCTGAGAGAGATCCGCTTCGCGGCACTCGCCCTGAGGCAAGTCCCTG 1313
 QY 1139 CTTTCAGGCTCTTGTATTAAGATTCGAATTAAGCCTTGTGTGAGAGACAGATGATGCA 1198
 DB 1314 CTCTCGGGGTGCTCAAGAGAGACCTACACAGAGGTGCTGGGGGCTCCGAGGATTC 1373
 QY 1199 AAGAAATTAATGAGACACAGTTCTTCTCTGAGTAACCTGGCAAGATGATATGATAA 1258
 DB 1374 AAGAGATCATGACGACCCGCTTCTTGGCCACATCGTGTGCGAGATGTATGAGAA 1433
 QY 1259 AAGCTGTACCTCTTTTAACCTCAAGTAACTGAGACAGATATCTGATATTTGAT 1318
 DB 1434 AAGCTGAGCCACCTTTCAGAGCCCGAGTACCTCTGAGACTGACACAGATATTCGAT 1493
 QY 1319 GAAGAATTT-ACAGCTCAGACTATTAACAATTAACACCACTGAATAA 1363
 DB 1494 GAGGAGTTTCAGAGCTCAGATGATCAACATCAAGCCGCTGATCAA 1539

RESULT 11
 CK781668 787 bp mRNA linear EST 23-FEB-2004
 LOCUS UI-M-HE0-cma-g-07-0-UI.r1 NIH_BMAP_HE0 Mus musculus cDNA clone
 DEFINITION IMAGE:30629430 5', mRNA sequence.
 CK781668
 VERSION CK781668.1 GI:42747346
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 787)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@os-r@mail.nih.gov
 Tissue Procurement: Dr. James Ian Unive
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouse1.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.

FEATURES

source

1..787
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30629430"
 /tissue_type="whole eye"
 /dev_stage="embryo 12.5,13.5,14.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1lb="NIH BMAP HE0"
 /note="Organ: Eye; Vector: pYX-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 Bonaudo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TTAATGAGT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH)."

ORIGIN

Query Match 45.2%; Score 698.6; DB 7; Length 787;
 Best Local Similarity 95.3%; Pred. No. 1.8e-171;
 Matches 752; Conservative 0; Mismatches 34; Indels 3; Gaps 3;

QY 13 GAGCGATGTACCATTTGAAAGAGGCTGGGTCGAAAGAGGGGGAATATATAAAAA 72
 DB 1 GAGCGATGTACCATTTGAAAGAGGCTGGGTCGAAAGAGGGGGAATATATAAAAA 60
 QY 73 CTGAGAGCAAGATACCTCTTTTGAAGACAGATGCTCATATGATATATAAGAA 132
 DB 61 CTGAGAGCAAGATACCTCTTTTGAAGACAGATGCTCATATGATATATAAGAA 120
 QY 133 ACCTCAAGATGTGATTTACCTTATCCCTCAACAACTTTTCAATGTGGCAAAATGTCAGTT 192
 DB 121 ACCTCAAGATGTGATTTACCTTATCCCTCAACAACTTTTCAATGTGGCAAAATGTCAGTT 180
 QY 193 AATGAAAAAGAAAGCAAGCAAGCAAAAGCAATTTAATCAGATGTCAGTGGACTAG 252
 DB 181 AATGAAAAAGAAAGCAAGCAAGCAAAAGCAATTTAATCAGATGTCAGTGGACTAG 240
 QY 253 TGTATAGAGAGAAACATTTTATGTAGATATCTCAGAGAAAGGAAATGACAGAAAC 312
 DB 241 TGTATAGAGAGAAACATTTTATGTAGATATCACCAGAGAAAGGAAATGAGACGGAAG 300
 QY 313 TATCAGGCTGTAGCAGACAGACTGACAGGCAAGAGAGAGAGATGATTTGTATCC 372
 DB 301 TATCAGGCTGTAGCAGACAGACTGACAGGCAAGAGAGAGATGATTTGTATCC 360
 QY 373 AACTTCACAAATTTGAATATATGAGAGAGAGATGATGCTTCACAAACCATCATTA 432
 DB 361 AACTTCACAAATTTGAATATATGAGAGAGAGATGATGCTTCACAAACCATCATTA 420
 QY 433 AAGAAAGCAATGATGATTTTGAATTTGAACTACTAGTAAAGGACATTTGGGAA 492
 DB 421 AAGAAAGCAATGATGATTTTGAATTTGAACTACTAGTAAAGGACATTTGGGAA 480
 QY 493 AGTTATTTTGGTTTCGAGAGAGGCAAGTGAATAATCTATGCTATGAAGATTTGAA 552
 DB 481 AGTTATTTTGGTTTCGAGAGAGGCAAGTGAATAATCTATGCTATGAAGATTTGAA 540
 QY 553 AGAAGCATTTATTTGCAAGAGATGAGTGGCACACTTACCTGAAGAGAGATTA 612
 DB 541 AGAAGCATTTATTTGCAAGAGATGAGTGGCACACTTACCTGAAGAGAGATTA 600
 QY 613 GAACACTAGACATCCCTTTTAAACATCCTTGAATATTTCTTCCAGACAAAGACGTT 672
 DB 601 GAACACTAGACATCCCTTTTAAACATCCTTGAATATTTCTTCCAGACAAAGACGTT 660
 QY 673 GTGTTTGTGATGAAATATGTTAATGGGGCGAGCTGTTTTCATTTGTGAGAGAGCG 732
 DB 661 GTGTTTGTGATGAAATATGTTAATGGCGAGAGCTGTTTTCATTTGTGAGAGAGCG 719
 QY 733 GGTGTTCTGTGAGAGCCGCAACGTTTCTATGTCGAGAAATTTGCTGCTGGAGCA 792
 DB 720 GATGTTCTGTGAGAGCGCAACGTTTCTATGTCGAGAAATTTGCTGCTGGAGCA 777
 QY 793 TCTACATTC 801
 DB 778 TCTACATTC 786

RESULT 12
 BU703964 766 bp mRNA linear EST 15-JUL-2003
 LOCUS UI-M-FO0-byr-1-04-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
 DEFINITION IMAGE:6406347 5', mRNA sequence.
 ACCESSION BU703964
 VERSION BU703964.1 GI:23631576
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chih, Ph.D., program coordinator."

ORIGIN

Query Match 44.8%; Score 695; DB 6; Length 759;
Best Local Similarity 94.7%; Pred. No. 1,6e-170;
Matches 719; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 91 CCTTTGAGACAGATGGCTCATTCATAGATATTAAGAGAAACCTCAGATGTGATTT 150
Db 1 CTTTGAAGACAGATGGCTCATTCATAGGCTATTAAGAGAAACCTCAGATGTGACTT 60

QY 151 ACCTTATCCCTTCAACCACTTTTCAGTGGCAAAATGCCAGTTAATGAAAACAGACACC 210
Db 61 ACCTTATCCCTTCAACCACTTTTCAGTGGCAAAATGTCACTTATGAAAACAGACACC 120

QY 211 AAGCCAAACACATTTTATTCAGATGCTCCAGTGGACTACTGTTATAGAGAAACATT 270
Db 121 AAGCCAAATACATTTTATTCAGATGCTCTTCAGTGGACCACTGTTATAGAGAAACATT 180

QY 271 TCATGTAGATATCTCCAGAGAAAGGAGAGATGAGACAGAACTATCCAGGCTGTAGACA 330
Db 181 TCATGTAGATATCACAGAGAGAAAGAGAGATGAGACAGAACTATCCAGGCTGTAGACA 240

QY 331 CAGACTGCAAGGCAAGAGAGAGAGAGATGATTTGATGCTCACTTCAAAATTTGATA 390
Db 241 CCATTTGCAAGGCAAGAGAGAGAGAGATGATTTGATGCTCACTTCAAAATTTGATA 300

QY 391 TATAGAGAGAGAGAGATGATGCTTACACCCATCATTAAGAGAAAGCAATGATGA 450
Db 301 TATAGAGAGAGAGAGATGATGCTTACACCCATCATTAAGAGAAAGCAATGATGA 360

QY 451 TTTTGAATTTTGAATCTAGATTAAGGCACTTTTGGAAAGTTATTTGGTTGAGAGA 510
Db 361 TTTTGAATTTTGAATCTAGATTAAGGCACTTTTGGAAAGTTATTTGGTTGAGAGA 420

QY 511 GAAGGCAAGTGAAGAAATCTATGCTATGAAGATTTGAGAGAAAGAGCTATTTGCAAA 570
Db 421 GAAGGCAAGTGAAGAAATCTATGCTATGAAGATTTGAGAGAAAGAGCTATTTGCAAA 480

QY 571 GGATGAAGTGGCAACCTCTAATGAAGAGAGATTTAAGAAACCTAGACATCCCTT 630
Db 481 GGATGAAGTGGCAACCTCTAATGAAGAGAGATTTAAGAAACCTAGACATCCCTT 540

QY 631 TTTAACAATCTTGAATAATATCTTCCAGACAAAGACCGTTTGTGTTTGTGATGATA 690
Db 541 TTTAACAATCTTGAATAATATCTTCCAGACAAAGACCGTTTGTGTTTGTGATGATA 600

QY 691 TGTTAATGSGGCGAGCTGTTTTCATTTTGTGAGAGACCGGCTTCTGAGACCG 750
Db 601 TGTTAATGSGGCGAGCTGTTTTCATTTTGTGAGAGACCGGCTTCTGAGACCG 660

QY 751 CACAGCTTCTATGSGGCAAAATGTGCTGCTGCGACTATCTCATTTCCGGAAGAT 810
Db 661 CACAGCTTCTATGSGGCAAAATGTGCTGCTGCGACTATCTCATTTCCGGAAGAT 720

QY 811 TGTGTACCGTATCTCAAGTTGAGAGATCTAATGCTGGA 849
Db 721 TGTGTACCGTATCTCAAGTTGAGAGATTTGATGCTAGA 759

RESULT 14
CK639280 760 bp mRNA linear EST 28-JAN-2004
LOCUS
DEFINITION UT-M-H00-cmx-d-16-0-UT.r1 NIH_BMAP_H00 Mus musculus cDNA clone

IMAGE:30637815 5', mRNA sequence.
CK639280
CK639280.1 GI:41365146
EST.
SOURCE
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 760)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source

Seq primer: pYX-5.

Location/Qualifiers

1..760
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/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NIH BMAP H00"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Honaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGACTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Query Match 44.8%; Score 692.8; DB 7; Length 760;
Best Local Similarity 94.5%; Pred. No. 6e-170;
Matches 718; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 195 TGAAGACAGAGACCAAGCCAAACACATTTATATCAGATCTCCAGTGAATACAG 254
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QY 255 TTATAGAGAGACATTTCAATGATATCTCCAGAGAGAGAGAGATGAGATGATGATCA 314
Db 61 TTATAGAGAGACATTTCAATGATATCTCCAGAGAGAGAGAGATGAGATGATGATCA 120

QY 315 TCCAGGCTGTAGACAGACATGCGAGAGCAAGAGAGAGAGATGAAATTTGATGCCA 374
Db 121 TCCAGGCTGTAGCGCGACGATGCGAGAGCAAGAGAGAGAGATGAAATTTGATGCCA 180

QY 375 CTTCAAAATTTATATATATAGAGAGAGAGATGATGATGATGATGATGATGATGAT 434
Db 181 CTTCAAAATTTATATATATATAGAGAGAGAGATGATGATGATGATGATGATGATGAT 240

QY 435 GAAAGACATGATGATTTTGAATTTGATGATGATGATGATGATGATGATGATGATGAT 494
Db 241 GAAAGACATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATG 300

QY 495 TTATTTGGTTCAGAGAAAGGCAAGTGAATACTATGTAAGATTCTGAAGAAAG 554
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 DB 361 AAGTCTATTTCAGAAAGATGAAGTGGCACACTCTTAACCTGAAGACAGATTAAGA 420
 QY 615 ACACCTAGATCCCTTTTAACATCCTTGAATAATTCCTCCGACAAAGACCGTTGT 674
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 QY 675 GTTTTGTGATGAATATGTTAATGAGGAGAGCTGTTTTCCATTGTCAGAGAGCGG 734
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 DB 721 CCATGAAGACATTTCTGTGCACTCCGAAGTACTGCGACC 760

RESULT 15
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 DEFINITION UI-M-FYO-cfb-h-05-0-UI.x1 NIH_BMAP_FYO Mus musculus cDNA clone
 ACCESSION CB525973
 VERSION CB525973.1 GI:29359446
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 746)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouseefi.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

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 /db_xref="taxon:10090"
 /clone="IMAGE:6847254"
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 /dev_stage="embryo 13.5, 14.5, 16.5, 17.5 sdp"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_id="NIH_BMAP_FYO"
 /note="Organ: Brain; Vector: pYX-Anc; Site_1: Ecor I;"

Site 2: Not I; The library was constructed according
 Bonaldo, Lemmon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Anc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCGAGACAG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
 Developing Mouse Nervous System", supported by National
 Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 43.8%; Score 677.4; DB 6; Length 746;
 Best Local Similarity 94.2%; Pred. No. 6.5e-166;
 Matches 702; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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 DB 1 AGAAACCTCAAGATGAGATTACCTTATCCCTCAACAACCTTTCAAGTGGCAAAATGCC 60
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 QY 249 CTACTGTTTATAGAGAAACATTTTCATGTAATCTCCAGAGAAAGGAAATGACAG 308
 DB 121 CCAGTGTATATAGAGAAACATTTTCATGTAATCTCCAGAGAAAGGAAATGACAG 180
 QY 309 AAGCTATCCAGGCTGTAGACAGACAGCTGACAGAGCAAGAAAGAGAGAAATGTA 368
 DB 181 AAGCTATCCAGGCTGTAGACAGACAGCTGACAGAGCAAGAAAGAGAGAAATGTA 240
 QY 369 GTCCAACTTCACAAATGTAATATATAGAGAGAAAGAGATGATGCTTCAACCCATC 428
 DB 241 GCCCAACCTTCACAAATGTAATATATAGAGAGAAAGAGATGATGCTTCAACCCATC 300
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 DB 301 ATTAAGAAAGACATGTAATGTTTGAATATTTGAATCTAGTAAAGCACTTTTG 360
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 DB 361 GGAAGTATTTTGGTTCAGAGAAAGGCAAGTGAATACTATGTAAGATTCTGA 420
 QY 549 AGAAAGAGTCAATTTGCAAAAGATGAAGTGGCACACACTCTTAACCTGAAGAGAT 608
 DB 421 AGAAAGAGTCAATTTGCAAAAGATGAAGTGGCACACACTCTTAACCTGAAGAGAT 480
 QY 609 TAAAGAACCTAGACATCCCTTTTAAACATCTTGAATATTTCTCCAGACAAAGACC 668
 DB 481 TAAAGAACCTAGACATCCCTTTTAAACATCTTGAATATTTCTCCAGACAAAGACC 540
 QY 669 GTTTGTTTGTGATGAATATGTTAATGAGGAGAGAGCTGTTTTCCATTGTCGAGAG 728
 DB 541 GTTTGTTTGTGATGAATATGTTAATGAGGAGAGAGCTGTTTTCCATTGTCGAGAG 600
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 DB 601 AGCGGATGTTCTGAGAGACGACACGTTTCTATAGTGCAGAAATGTCCTGCTGG 660
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 QY 849 ACAAAAGGCGACATTAATAATTTAC 873
 DB 721 ATTAAGATGGCCATTAATAATTTAC 745

Search completed: April 13, 2005, 07:31:18
Job time : 4728 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 13, 2005, 06:12:34 ; Search time 5103 Seconds
(without alignments)
4346.314 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558
Sequence: 1 MSDVITVKEGWQKGEYIK.....MNERPRHPPEPSYASGRE 479

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO.spool.p/US09869079/runat.11042005.190023.13438/app.query.fasta_1.647
-DB=GenEmbl -QFMT=fasterp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09869079@cgn2.1.15600@runat.11042005.190023.13438 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_hc:.*
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14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2558	100.0	1440	6	BD142211 Method to
2	2558	100.0	1440	12	AY335691 Synthetic
3	2558	100.0	1547	6	BD251226 Human Akt
4	2558	100.0	1547	6	AX026529 Sequence

5	2558	100.0	1547	9	HSA245709	AJ245709 Homo sapi
6	2558	100.0	1706	9	AF085234	AF085234 Homo sapi
7	2558	100.0	1708	9	AF124141	AF124141 Homo sapi
8	2558	100.0	2367	6	BD260777	BD260777 Human pro
9	2558	100.0	2811	9	AF135794	AF135794 Homo sapi
10	2545	99.5	1436	6	BD251227	BD251227 Human Akt
11	2545	99.5	1436	6	AX026530	AX026530 Sequence
12	2543	99.4	1760	10	AF124142	AF124142 Mus muscu
13	2533	99.0	4751	10	BC066861	BC066861 Mus muscu
14	2480	97.0	1551	6	CQ714620	CQ714620 Sequence
15	2402	93.9	1570	6	BD250154	BD250154 AKT nucle
16	2402	93.9	1570	6	AX056819	AX056819 Sequence
17	2402	93.9	1570	6	AX251592	AX251592 Sequence
18	2402	93.9	1584	9	HSMB01048	AL117525 Homo sapi
19	2402	93.9	1595	9	AY005799	AY005799 Homo sapi
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21	2146.5	83.9	2277	5	AF039943	AF039943 Gallus ga
22	2113	82.6	1808	5	AF317656	AF317656 Xenopus 1
23	2105.5	82.3	1443	12	AY335629	AY335629 Synthetic
24	2105.5	82.3	2729	9	BC000479	BC000479 Homo sapi
25	2105.5	82.3	2868	9	BC084538	BC084538 Homo sapi
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30	2100.5	82.1	2701	10	BC066018	BC066018 Mus muscu
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33	2099.5	82.1	1443	6	A84455	A84455 Sequence 70
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36	2099.5	82.1	2181	6	AX427354	AX427354 Sequence
37	2099.5	82.1	2181	6	BD082540	BD082540 A method
38	2099.5	82.1	2184	6	A84523	A84523 Sequence 13
39	2099.5	82.1	2184	6	CQ830047	CQ830047 Sequence
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41	2099.5	82.1	2184	6	AX427422	AX427422 Sequence
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43	2099.5	82.1	2610	6	A62733	A62733 Sequence 1
44	2099.5	82.1	2610	6	A63232	A63232 Sequence 3
45	2099.5	82.1	2610	6	AR076381	AR076381 Sequence

ALIGNMENTS

RESULT 1	BD142211	1440 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD142211				
DEFINITION	Method for controlling apoptosis and polypeptide controlling				
ACCESSION	BD142211				
VERSION	BD142211.1	GI:223237156			
KEYWORDS	WO 0215925-A/5.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	Tsuruo, T., Fujita, N. and Sato, S.				
JOURNAL	1 (bases 1 to 1440)				
COMMENT	Method for controlling apoptosis and polypeptide controlling				
	Patent: WO 0215925-A 5 28-FEB-2002;				
	KYOWA HAKKO KOGYO CO LTD, TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO				
	OS Homo sapiens (human)				
	PN WO 0215925-A/5				
	PD 28-FEB-2002				
	PF 22-AUG-2001 WO 2001JP007179				
	PI 22-AUG-2000 JP 00P 251529				
	PC TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO				
	PC A6IK38/17, A6IK38/45, A6IK39/395, A6IK45/00, A6IP43/00, A6IP3/08,				
	PC A6IP43/00, C07K7/04, C07K14/47, C07K16/18, C12N1/15, C12N1/19 PC				
	PC C12N1/21, C12N5/10,				
	PC C12P21/02, C12N15/09, G01N33/50, G01N33/15, G01N33/566, G01N33/58				

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ORIGIN

Alignment Scores:

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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-869-079B-3 (1-479) x BD142211 (1-1440)

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 QY 81 ThrValIleGluIYsThrPheIleValAspThrProGluIYsGluIYTrPThrGlu 100
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 Synthetic construct Homo sapiens v-akt murine thymoma viral
 oncogene-like 3 (AKT3) mRNA, partial cds.
 ACCESSION
 AY335691
 VERSION
 AY335691.1 GI:33304020
 KEYWORDS
 FLI CDNA.
 SOURCE
 synthetic construct
 ORGANISM
 other sequences; artificial sequences.
 1 (bases 1 to 1440)
 2 (bases 1 to 1440)
 TITLE
 Cloning of human full-length CDS FLEXGene kinases in
 recombinational vector system
 JOURNAL
 Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,
 Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E.,
 Labaer,J., and Brizuela,L.
 Direct Submission
 Submitted (02-JUN-2003) Biological Chemistry and Molecular
 Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
 Cambridge, MA 02141-2023, USA
 This CDS clone is a part of a collection of human full-length
 expression clones generated by Harvard Institute of Proteomics.
 Each CDS has been cloned without stop-codon (to allow fusion with

C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.

FEATURES

source

Location/Qualifiers
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1..21440
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/codon_start=1
/transl_table=1
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/protein_id="AA002518.1"
/db_xref="GI:33304021"

CDS

gene

ORIGIN

Alignment Scores:

Pred. No.: 3,736-213 Length: 1440
Score: 2558.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-869-079B-3 (1-479) x AY335691 (1-1440)

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1 ATGAGCGATGTTACCTTGTGAAGAGGTTGGGTTCAAGAGGAGGAGATATTAATA 60
21 AantTPArGProArGTYrPheLeuLeuLysThrAspGlySerPheIleGlyTyrIlyGlu 40
61 AACTGGAGGCCAAGATACTTCTTTGAAGACGATGGCTCATTCATAGATATAAAGG 120
41 LysPProGlnAspValAspLeuProTYrProLeuAsnAsnPheserValAlaLysCysGln 60
121 AAACCTCAAGATGTGATTACCTTATCCCTCAACAACTTTCACTGCGCAAAATCCCG 180
61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyrThr 80
181 TTAAATGAAGAAACGAGACCAAGCCAAACACATTTATATCATGATGTCTCCAGTGA 240
81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTyrThrGlu 100
241 ACTGTTATAGAGAAATTTATCATGTAGATATCTCCAGAGGAAAGGAAATGACAGAA 300
101 AlaIleGluAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetLysCysSer 120
301 GCTATCCAGGCTGTACAGACAGACTGCAGAGGCAAGAGAGGAAATGAAATGTAGT 360
121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHisHis 140

361 CCAACTTCACAAATTGATATATAGAGAGAAAGATGATGCTCTACAAACCATCAT 420
141 LysAlaGlySerThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
421 AAAGAGAAACATGATGATATTTTGAATCTTATGAAACATCACTAGTAAAGCACTTTGGG 480
161 LysValIleLeuValArgGluLysValAspGlyLysTyrTyrAlaMetLysIleLeuLys 180
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DEFINITION Human Akt-3.
ACCESSION BD251226
VERSION BD251226.1 GI:33060996
KEYWORDS JP 2002535964-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1547)
AUTHORS Masure, S.L.J. and Richardson, A.
TITLE Human Akt-3.
JOURNAL Patent: JP 2002535964-A 1 29-OCT-2002;
JANSSEN PHARMA/CEUTICA NV
OS Homo sapiens (human)
PN JP 2002535964-A/1
PD 29-OCT-2002
PF 17-DEC-1999 JP 2000589669
PR 22-DEC-1998 GB 9828375.7
PI STEFAN LEO JOZEF MASURE, ALAN RICHARDSON
PC C12N15/09, A61K31/713, A61K38/53, A61K39/395, A61K39/395, A61K48/00, PC A61P35/00.
PC A61P43/00, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/12, C12Q1/02,
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 REFERENCE
 1 Masure, S.L. and Richardson, A.
 AUTHORS Human akt-3
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 JOURNAL MASURE, STEPHAN LEO JOZEF (BR) ; RICHARDSON ALAN (BE) ; JANSSEN
 PHARMACEUTICA NV (BE)
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 1 Masure, S., Haefner, B., Weselink, J.J., Hofnagel, E., Mortier, E.,
 Verhaesele, P., Tytelaars, A., Gordon, R. and Richardson, A.
 TITLE Molecular cloning, expression and characterization of the human
 serine/threonine kinase Akt-3
 JOURNAL Eur. J. Biochem. 265 (1), 353-360 (1999)
 MEDLINE 99421751

PUBMED 10491192
 REFERENCE 2 (bases 1 to 1547)
 AUTHORS Masure, S.L.
 TITLE Direct Submission
 JOURNAL Submitted (25-AUG-1999) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beersse, BELGIUM
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ACCESSION AF085234
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1706)
Li,X., Yu,L., Huang,H., Zhang,M., Zhao,Y. and Zhao,S.
Cloning of a novel human cDNA, STK-2, which encodes a rat
serine-threonine protein kinase (STK) homolog
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1706)
Zhao,Y.
REFERENCE Direct Submission
AUTHORS Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan
JOURNAL University, Lab of Human Gene Research, No. 220, Handan Road,
Shanghai, People's Republic of China, 200433
LOCATION/Qualifiers
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ORIGIN
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US-09-869-079b-3 (1-479) x AF085234 (1-1706)

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ACCESSION AF124141
VERSION AF124141.1 GI:4757578
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1708)
AUTHORS Brodebeck,D., Cron,P. and Hemmings,B.A.
TITLE A human protein kinase Bgamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain
JOURNAL J. Biol. Chem. 274 (14), 9133-9136 (1999)
MEDLINE 99194749
PUBMED 10092583
REFERENCE 2 (bases 1 to 1708)
AUTHORS Brodebeck,D., Cron,P. and Hemmings,B.A.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerallee 66, Basel 4058, Switzerland
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ORIGIN
Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-869-079B-3 (1-479) x AF124141 (1-1708)
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ACCESSION	BD260777		
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KEYWORDS	JP 2002539823-A/1.		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2367)		
TITLE	Altersand, A.		
JOURNAL	Human protein kinase B-gamma polypeptide and method of degrading nonhuman protein kinase B-gamma		
COMMENT	Patent: JP 2002539823-A 1 26-NOV-2002; BIOVITRUM AB		
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	PN JP 2002539823-A/1		
	PD 26-NOV-2002		
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	PR 25-MAR-1999 SE 990115-7		
	PI ANNEI ALTERSAND		
	PC C12N15/09,A01K67/027,C07K16/40,C12N1/15,C12N1/19,C12N1/21,PC C12N5/10,		
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VERSION AF135794.1 GI:4574743
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Nakatani, K., Sakaue, H., Thompson, D.A., Weigel, R.J. and Roth, R.A.
TITLE Identification of a human AKT3 (protein kinase B gamma) which
contains the regulatory serine phosphorylation site
JOURNAL Biochem. Biophys. Res. Commun. 257 (3), 906-910 (1999)
MEDLINE 99225329
PUBMED 10208883
REFERENCE
2 (bases 1 to 2811)
Thompson, D.A., Nakatani, K. and Sakaue, H.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Surgery, SMLS Building, Room P228, 1201
Welch Road, Stanford, CA 94305, USA
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ORIGIN
Alignment Scores:
Pred. No.: 8.17e-213 Length: 2811
Score: 2558.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-869-079B-3 (1-479) x AF135794 (1-2811)

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Db 61 AACTGAGGCCAAGATATCTCTTTTGAAGACAGATGGCTCATTTGATGATATTAAGG 120
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Db 301 GCTATCCAGGCTGTGACAGACAGACTGCAGAGGCAAGAGAGAGATGATATGTAGT 360
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QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
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Db 1021 TGTGGAGAGTTACCTTTCTACACACAGACCATGAGAAACTTTGAAATTAATATTAATG 1080
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QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerLysLeu 380
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QY 421 ProPheLyPProGInaIAlThiSerGlyuThraSpThraGlyrPheAspGlyGluPheThr 440
DB 1261 CCTTTAAACCTCAAGTAAATCTGAGACAGATACATGATATTTGATGAAGATTATTA 1320
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RESULT 10
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LOCUS BD251227 Human Akt-3.
DEFINITION BD251227
ACCESSION BD251227.1 GI:33060997
VERSION JP 2002535964-A/2.
KEYWORDS JP 2002535964-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1436)
AUTHORS Masure,S.L.J. and Richardson,A.
JOURNAL Human Akt-3
Patent: JP 2002535964-A 2 29-OCT-2002;
JANSSEN PHARMACEUTICA NV
OS Homo sapiens (human)
PN JP 2002535964-A/2
PD 29-OCT-2002 JP 2000589669
PF 17-DEC-1999 JP 2000589669
PR 22-DEC-1998 GB 9828375.7
PI STEFAN LEO JOZEF MASURE,ALAN RICHARDSON
PC C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K39/395,A61K48/00,PC
A61P35/00,
PC A61P43/00,C07K16/40,C12N1/15,C12N1/19,C12N1/22,C12N5/10,C12N9/
PC 12,C12Q1/02,
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1.1435
1.1435
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Alignment Scores:
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Score: 2545.00 Matches: 477
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Best Local Similarity: 99.79% Mismatches: 1
Query Match: 99.49% Indels: 0
DB: 6 Gaps: 0
US-09-869-079B-3 (1-479) x BD251227 (1-1436)
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QY 61 LeuMetLySthrGlyuArgProLySProAenThrPheIleIleArgCysLeuGlnTPhr 80
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DB 421 AAAGAAACACATGATGATATTGACTATTGAAACTCTAGTMAAGCACTTTGGG 480
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QY 221 LeuCySPheValaMetGlyuTyrrValaAsnGlyuGlyuLeuPheHisleuSerArgGlu 240
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QY 261 TyrrLeuHisSerGlyuLySleValTyrrArgAspLeuLySleuGluAsnLeuMetLeuAsp 280
DB 781 TATCTACATTCGCGAAAGATGTGTACCGTGATCTCAAGTTGAGAGATTAATGCTGAGAC 840
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 Db 1321 GCTCAGACTATTACATAACACCACTGAAAAATATGATGAGATGTGACCTGCATG 1380
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RESULT 11

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 LOCUS AX026530 Sequence 2 from Patent WO0037613.
 DEFINITION AX026530
 ACCESSION AX026530
 VERSION AX026530.1 GI:10187718
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Masure, S.L. and Richardson, A.
 AUTHORS Human akt-3
 TITLE Patent: WO 0037613-A 2 29-JUN-2000,
 JOURNAL MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
 PHARMACEUTICA NV (BE)

FEATURES
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ORIGIN

Alignment Scores:

Pred. No.: 5 04e-212 Length: 1436
 Score: 2545.00 Matches: 477
 Percent Similarity: 99.79% Conservative: 0
 Best Local Similarity: 99.79% Mismatches: 1
 Query Match: 99.49% Indels: 0
 DB: 6 Gaps: 0

US-09-869-079b-3 (1-479) x AX026530 (1-1436)

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QY 461 ASDASGLUARGARProHisPheProGluPheSerTyrSerAlaSerGlyArg 478
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RESULT 12
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DEFINITION AF124142
ACCESSION AF124142 GI:4757580
VERSION AF124142.1
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 1760)
TITLE Brodebeck, D., Cron, P. and Hemmings, B.A.
A human protein kinase Bgamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain
JOURNAL 3 Biol. Chem. 274 (14), 9133-9136 (1999)
MEDLINE 99194749
PubMed 10092583

REFERENCE
AUTHORS 2 (bases 1 to 1760)
TITLE Brodebeck, D., Cron, P. and Hemmings, B.A.
Direct Submission
JOURNAL Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerstrasse 66, Basel 4058, Switzerland
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 9.55e-212 Length: 1760
Score: 2543.00 Matches: 477
Percent Similarity: 99.79% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 1
Query Match: 99.41% Indels: 0
DB: 10 Gaps: 0

US-09-869-079b-3 (1-479) x AF124142 (1-1760)

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QY 221 LeuCysPheValMetGluTyrValAlaGlnGlyGluLeuPhePheHisLeuSerArgGlu 240
DB 697 TTGTGTTTGTATGGAATATGTAATGCGAGACACTGTTTTCATTTGCGAAGAG 756

QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGlnIleValSerAlaLeuAsp 260
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QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 817 TATCTCATTTGGAAGAAAGATGTGTACCTGATCTCAAGTTGGAGAAATTTAGATGAT 876

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DB 877 AAGAGAGGCAATATAAAATTAACGATTTTGGCTTTGCAAGAAAGGATCAACAGATGCA 936

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DB 937 GCTACCATGAGACATTTCTGTGGCACACAGATACCTGGCACACAGGTATTAGAAAT 996

QY 321 AsnAspTyrGlyArgAlaValAspTyrTyrGlyLeuGlyValAlaMetTyrGluMetMet 340
DB 997 AATGACTTAAGCGCGAGCGGTGACGTGGGCTTAGGTGTATGATGAATATGATG 1056

QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
DB 1057 TGTGAAAGGTTGCTTTCTACAAACGAGATCATGAAAACTTTTGAATTAATACAAAG 1116

QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
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QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMet 400
DB 1177 TTGATTAAGATCAAAATTAACGCTTGTGTGAGGCGCGAGATGATCAAAAGAAATCATG 1236

QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLysLeuValPro 420
DB 1237 AGGCAATGATTTTTTCTCGAGTAAACGTGCAAGATGTATATGACAAAAAGCTTGACCT 1296

QY 421 ProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440

FEATURES	REMARK	COMMENT
Db	1297	CCTTTTAAGCCTCAAGTAACATCTGAAACAGACCCGATATTGTAAGAAATTACA 1358
Oy	441	AlaGlnThrIleThrIleThrProProGluysrYrAspGluAspGlyMetAspCysMet 460
Db	1357	GCTCAGACTATTATCAATAACACACACTGAAAAAGTATGACGACGACGCGATGACGCGCATG 1416
Oy	461	AspAsnGluYrGArGyrProHisPheProGlnPheSerYrSerAlaSerGlyYrArgGlu 479
Db	1417	GACAAACGAGCGCGCGCACACTTCCCTCAAGTCTCTACTCTGCAAGCGGACGGGAA 1473
RESULT 13		
BC066861		4751 bp mRNA linear ROD 30-JUN-2004
LOCUS		Mus musculus thymoma viral proto-oncogene 3, mRNA (cDNA clone
DEFINITION		MG:76721 IMAGE:30089997), complete cds.
ACCESSION		BC066861
VERSION		BC066861.1 GI:45219866
KEYWORDS		MGC.
SOURCE		Mus musculus (house mouse)
ORGANISM		Mus musculus
REFERENCE		Euhay/Ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4751)
AUTHORS		Strauberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Ditschenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schaefer,T.E., Brownstein,M.J., Udell,T.B., Toobylnki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McKwan,P.J., McKeernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S.C., Garcia,A.M., Gay,L.J., Hulyk,S.W., Valladao,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahney,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bonfield,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butcherfield,Y.S., Krzywnicki,M.I., Skalska,U., Smalins,D.E., Scherf,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE		Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED		12477932
REFERENCE		2 (bases 1 to 4751)
AUTHORS		Strauberg,R.
TITLE		Direct Submission
JOURNAL		Submitted (01-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK		NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT		Contact: MGC help desk Email: cgasbs-re@mail.nih.gov Tissue Procurement: Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy) cDNA Library Preparation: Yulan Piao and Minoru Ko (National Institute on Aging, NIH: http://1gsun.grc.nia.nih.gov/cDNA/) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdbpaxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 144 Row: e Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753031.
Location/Qualifiers

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ORIGIN

Alignment Scores:
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Score: 2533.00 Matches: 475
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Best Local Similarity: 99.16% Mismatches: 2
Query Match: 99.02% Indels: 0
DB: 10 Gaps: 0

US-09-869-079B-3 (1-479) x BC066861 (1-4751)

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Db 107 AACGAGGAGCCCAAGATATCTTCCTTTTGAAGACATGGCTCATTCATAGGCTATAAGAGAG 166
QY 41 LysProGlnAspValAspLeuProTYrProLeuAsnAsnPheSerValAlaLysCysGln 60
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QY 81 ThrValIleGluArgThrPheIleValAspThrProGluGluArgGluGluYrTrpThrGlu 100
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QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnIyGluGluArgMetAsnCysSer 120
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QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
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DEFINITION Sequence 554 from Patent WO02068579.
ACCESSION CQ714620

VERSION CQ714620.1 GI:42275477
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
JOURNAL Patent: WO 02068579-A 554 06-SEP-2002;
PE Corporation (NY) (US)
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ACCESSION BD250154
VERSION BD250154.1 GI:33059924
KEYWORDS JP 2002539781-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1570)
Guo,K., Pagnoni,M.F., Clark,K.L. and Ivashchenko,Y.D.
AKT nucleic acids, polypeptides, and uses thereof
Patent: JP 2002539781-A 1 26-NOV-2002;
AVENTIS PHARMACEUTICALS PRODUCTS INC
OS Homo sapiens (human)
PN JP 2002539781-A/1
PD 26-NOV-2002
PF 14-MAR-2000 JP 2000606725

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Db 906 TATCTACATTCGGAAGATGTGTACCGTATCTCAAGTTGGAGAAATCTAAATGCTGGAC 965
QY 281 LysAspGlyHisIleuValIleuThrAspPheGlyLeuCyapGluGlyIleuThrAspAla 300
Db 966 AAGATGGCCACATAAATAATTAAGATTTTGGACTTTGCAGAGAGGATCACAGATGCA 1025
QY 301 AlaThrMetLeuThrPheCyapGlyThrProGluTyrLeuAlaProGluValIleuGluAsp 320
Db 1026 GCCACCATGAAGCATTTGTGTGACCTCCAGAAATATCTGGCACAGAGGTGTAGAAAGAT 1085
QY 321 AsnAspTyrGlyValArgAlaValAspTyrPheGlyLeuGlyValIleuMetTyrGluMetMet 340
Db 1086 AATGACTATGGCCGAGAGTAGACTGTGGGGCTTAGGGGTGTGCATGATGAAATGATG 1145
QY 341 CyapGlyArgLeuProPheTyrAsnGluAspHisGlyIleuPheGluLeuIleuMet 360
Db 1146 TGTGGAGGTTACTTCTTCAACACAGACCATGAGAACTTTTGAATTAATTTAATG 1205
QY 361 GluAspIleuPheProAlaGlnLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
Db 1206 GAAGACATTAATTTCTCGAACACTCTTTCAGATGCAAAATCATTTGCGGCTC 1265
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyIleuProAspAspAlaLysGluIleuMet 400
Db 1266 TTGATTAAGATCCAAATAAAGCCCTGTGTGAGAGACCAAGATGATGCAGAAAGAAATTATG 1325
QY 401 ArgHisSerPhePheSerGlyValAsnTyrPheGluAspValTyrAspLysLysLeuValPro 420
Db 1326 AGACACAGTTTCTTCTGTGAGTAACCTGGCAAGATGTATATGATAAAAGCTTGTACCT 1385
QY 421 ProPheLysProGlnValIleuSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
Db 1386 CCTTTTAAACCTCAAGTAACATCTGAGACAGATATGATATTTTGTATGAAGAAATTACA 1445
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
Db 1446 GCTCAGACTATTAACAATAACACACCTGAAAAAATGTCAGCAATCA-----GATGT 1496
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Search completed: April 13, 2005, 10:36:54
Job time : 5130 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 13, 2005, 04:22:03 ; Search time 644 Seconds

(without alignments)
4403.037 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558
Sequence: 1 MSDVTIVKSGWQKRGSEYIK.....MDNERPPHPQPSYSASGRE 479

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Egapop 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: genesegn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2558	100.0	1440	3	AAA62451	Aaa62451 Human Akt
2	2558	100.0	1440	6	ABL50839	Ab150839 Human Akt
3	2558	100.0	1547	3	AAA62450	Aaa62450 Human Akt
4	2558	100.0	1547	12	ADN71939	Adn71939 Human ser
5	2558	100.0	2367	3	AAC61592	Aac61592 DNA encod

6	2558	100.0	2811	10	ADC26888	Adc26888 DNA encod
7	2558	100.0	2811	13	ADG88265	Adg88265 Human 141
8	2550	99.7	3285	3	AAC77341	Aac77341 Human ORF
9	2402	93.9	1570	3	AAA96637	Aaa96637 DNA encod
10	2402	93.9	1570	4	AAH79025	Aah79025 Human Akt
11	2402	93.9	1570	4	AAA89262	Aaa89264 Human ser
12	2402	93.9	1570	12	ADG85244	Adg85244 Human Chr
13	2146.5	82.3	2277	12	ADN71941	Adn71941 Chicken s
14	2105.5	82.3	2533	13	ADG85348	Adg85348 Human tum
15	2105.5	82.1	2978	9	ACD44893	Accd44893 Human sig
16	2100.5	82.1	2626	6	AAA09078	Aaa09078 Wild type
17	2100.5	82.1	2626	6	AAD28550	Aad28550 Mouse Akt
18	2100.5	82.1	2626	10	ADC26885	Adc26885 DNA encod
19	2100.5	82.1	2626	12	ADP48780	Adp48780 Mouse Akt
20	2100.5	82.1	6891	12	ADL25356	Adl25356 ARKS re1a
21	2099.5	82.1	1443	6	ABL50837	Ab150837 Human Akt
22	2099.5	82.1	1443	10	ADP18631	Adp18631 Human Akt
23	2099.5	82.1	2181	2	AAV71037	Aav71037 PKB-green
24	2099.5	82.1	2184	2	AAV71086	Aav71086 Green flu
25	2099.5	82.1	2610	2	AAE67135	Aae67135 Human RAC
26	2099.5	82.1	2610	2	AAE64812	Aae64812 Human RAC
27	2099.5	82.1	2610	2	AAZ41177	Aaz41177 Human AKT
28	2099.5	82.1	2610	2	AAZ22190	Aaz22190 Human Akt
29	2099.5	82.1	2610	3	AAA09076	Aaa09076 Wild type
30	2099.5	82.1	2610	6	AAO28548	Aao28548 Human Akt
31	2099.5	82.1	2610	6	ABK84055	Abk84055 Human CDN
32	2099.5	82.1	2610	11	ADJ31880	Adj31880 Human CDN
33	2099.5	82.1	2610	12	ADL25354	Adl25354 Human ARK
34	2099.5	82.1	2610	12	ADP48782	Adp48782 Human Akt
35	2099.5	82.1	2610	13	ACN39762	Acn39762 Tumour-as
36	2004	78.3	1446	6	ABL50838	Ab150838 Human Akt
37	2004	78.3	1593	12	ADG84311	Adg84311 Human tum
38	2004	78.3	1593	13	ADQ86662	Adq86662 Human tum
39	2004	78.3	1593	13	ADQ83643	Adq83643 Human tum
40	2004	78.3	1593	13	ADQ85783	Adq85783 Human tum
41	2004	78.3	1593	13	ACN40577	Acn40577 Tumour-as
42	2004	78.3	1599	2	AAE71252	Aae71252 Mouse Akt
43	2004	78.3	1599	3	AAO08448	Aao08448 Human Akt
44	2004	78.3	1599	3	AAZ60814	Aaz60814 Nucleotid
45	2004	78.3	1599	10	ADC26887	Adc26887 DNA encod

ALIGNMENTS

RESULT 1	AAA62451	standard; cDNA; 1440 BP.
ID	AAA62451	
XX	AAA62451:	
XX		
DT	13-NOV-2000	(first entry)
XX		
DE	Human Akt-3 coding sequence.	
XX		
KW	Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytosolic;	
KM	apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;	
KW	chromosome 1q43-44; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..1440
FT		/tag= a
FT		/product= "Akt-3"
XX		
PN	WO200037613-A2.	
XX		
PD	29-JUN-2000.	
XX		
XX		
PF	17-DEC-1999;	99WO-GB004311.
XX		
PR	22-DEC-1998;	98GB-00028375.
XX		

Accession	Sequence	Length	Matches	Conservative	Mismatches	Indels	Gaps
XX	(JUNC) JANSSEN PHARM NV.						
XX	Maeure SLJ, Richardson A;						
XX	WPI, 2000-498840/44.						
DR	P-Psdb; AABI3393.						
XX							
PT	New human serine/threonine kinase protein and the polynucleotide encoding						
PT	the protein, useful for preparing a medicament for treating disorders						
PT	associated with human serine/threonine kinase protein activity,						
PT	especially cancer.						
XX							
PS	Claim 4; Fig 1; 61pp; English.						
XX							
CC	The present sequence is the coding region of the nucleotide sequence that						
CC	encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also						
CC	known as protein kinase B (PKB) or "related to A and C protein Kinase"						
CC	(RAC-PK). The gene encoding Akt-3 is located on human chromosome 1,						
CC	region q43-q44. A human hippocampal EST sequence that showed high						
CC	similarity to the rat RAC-Pigamma sequence was used to design primers for						
CC	3' rapid amplification of cDNA ends (3' RACE). The sequence obtained in						
CC	the first round of 3' RACE was used to design primers for a second round.						
CC	The complete sequence was then amplified from human hippocampal cDNA by						
CC	PCR using primers based on the product of the second round of 3' RACE.						
CC	Akt can inhibit apoptosis induced by detachment from the extracellular						
CC	matrix. The Akt-3 nucleic acid molecule and protein may be used as						
CC	medicaments for treating cancer. Agents which influence the activity of						
CC	Akt-3 protein, and so stimulate apoptosis, may also be used to treat						
CC	diseases associated with Akt-3						
XX							
SQ	Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;						
	Alignment Scores:						
	Pred. No.:	1.18e-258	Length:	1440			
	Score:	2558.00	Matches:	479			
	Percent Similarity:	100.00%	Conservative:	0			
	Best Local Similarity:	100.00%	Mismatches:	0			
	Query Match:	100.00%	Indels:	0			
	DB:	3	Gaps:	0			
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QY	1 MetSerAspValThrIleValIysGluGlyTyrPvalGlnIlyrArgIlyGlyTyrIleIys	20					
Db	1 AAGACGAGATTACCACTTGTGAAAGAGGTGGGTTGAGAAAGGGGAGAAATATATAAAA	60					
QY	21 AsnTPARQProARQTYrPheIeuIeuIySThAspGISeRPhelIlegIYrYIySGlu	40					
Db	61 AACTGAGGCCCAAGATCTCTTCCTTTGMAAGACAGATGGCTCATTCATAGATATAAAG	120					
QY	41 LysPProGInAspValAspIeuProTYrProIeuAsnAsnSeserValAlaIySvYsgIn	60					
Db	121 AAACCTCAAGATGTGGATTACCTTATCCCTCAACAACCTTTCAATGGCAAAATGCGAG	180					
QY	61 LeuMelIySThGlnArgProIySProAsnThPheIleIleIeRQvSleuGIINTPrThr	80					
Db	181 TTAATGAAAAACGAACGACCAAGCCAAACACATTATATATCATGATGTCTCCAGTGGACT	240					
QY	81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTyrThrGlu	100					
Db	241 ACTGTTATAGAGAGAACATTTCTATGTAGTACTCCAGAGAAAGGAGAGATGACAGAA	300					
QY	101 AlaIleGlnAlaValAlaAspArgIeuArgGluGluGluGluIuArgMetAsnCYSer	120					
Db	301 GGTATCCAGGCTGTAGCAGACAGATGCGAAGGCCAAGAGAGAGAAATGAATTGTAGT	360					
QY	121 ProThrSerGlnIleAspAsnIleGIyGluGluGluMetAspAlaserThrThrHis	140					
Db	361 CCAACTTCACAAATTCATATATAGAGAGAGAAAGATGATGATCCTTCAACACCATCAT	420					
QY	141 LysAArgIySThMetAsnAspPheAspTYrIleuIySleuIeuIyIySGIYrThrPheGly	160					
Db	421 AAAAGAAACAAATGATGATTTTGTACTATTATAACTATAGATTAAGGACATTTTGGG	480					

QY	161	LYSVALIILELEUVALARGGLULYVALISSEGGILYLYSEYTYRYAIAAMELYSIIIELEULYS	180
DB	481	AAAGTATATTGGTTGTCAGAGAAAGCAAGTGGAAAAATCATAGCTATGAGAAATTCCTGAAG	540
QY	181	LYSGILUVALIILEILEALALYASPGIVALAIAHISPHLEUTHRGUSERARVALLEU	200
DB	541	AAAGAAGTCATTAATTCGAAAGAGAAAGTGGCAACACTCTAACTGAAAGCAGATTTA	600
QY	201	LYSANTHRARGHISPROPHLEUTHSERLEULYSFYRSERPHEGINTHRYASPARG	220
DB	601	AAGAACAACCTGACACCTCCCTTTTAACTCTTGAAATAATTCCTCCGACACAAAAGACCGT	660
QY	221	LEUCYSPHEVALMETGILUTRYVALASNGVGLVGLULEUPHEPHISLEUSERARGLU	240
DB	661	TTGGTTTGTGATGGAAATATGTTAAATGGGGGCGAGCTGTTTTTCCATTGTGCAAGAGAG	720
QY	241	ARGVALPHESERGIUASPARGTHRARPHETRYGLVALAGIULVALISERIALLEUASP	260
DB	721	CGGGTGTTCTCTGAGGACCGGACACGTTTCTATGTCGACAAATATGTCTGCTGCTTGAC	780
QY	261	TYRLEUHSSEGGILYLYSILEVALTYRARGPSLEULYSLEUGLUAMLEUMELLEUASP	280
DB	781	TATCTCACTTCGCGAAAGATGTGTACCGATGATCTCAAGTGGAGAACTCAATCTGGAC	840
QY	281	LYSASPGIYHSIIIELYSIIETHASPPHEGLYLEUCYSLYSGILUGIYIETHASPAIA	300
DB	841	AAAGTGCGCCCAATAAAATTCACGAATTTTGACTTTGCCAANAGAGGATCACAGATGCA	900
QY	301	ALATHRECTLYSTHRPHCYEGILYTHRPROGLUTRYLEUALAPROGLUVALLEUGLUASP	320
DB	901	GCCACCATGAAAGACATTCGTGGGACCTCCGAATATCTGGGACACAGAGGTGTGAAGAT	960
QY	321	ASNAPRYTRGLYAAAGALAVALASPTTPTTGPLYLEULIYVALVIMETTYRGULUMETEC	340
DB	961	AATACTATATGCGCCAGACGATACGTGTGGGGCTTAGGGGTTGTCAAGTATGAATAATATG	1020
QY	341	CYSGILYARGLUEPPOPHETRYASNGIINASPHISGLULYSLEUPHEGLULEULEUMETEC	360
DB	1021	TGTGGAGGTACTCTTTCTACAAACAGACCAATGAGAACTTTTGAATTATATATATG	1080
QY	361	GLUASPIIIELYSPHEPROARGTHLEUSERSEIRASPAIALYSESRLEULEUSERGILYLEU	380
DB	1081	GAAGACATTAATATTTCTCGAAACACTCTTCACATGCCAAATCATTTGCTTCAGGGCTC	1140
QY	381	LEULILEYASPPROASNUYARXLEUGLYGLVGLYPROASPARPAIALYSGIULILEMEC	400
DB	1141	TTGATPAAGGATCCAAATPAACGGCTTGGTGGAGAACCAAGATGATGCANAGAAATTAATG	1200
QY	401	ARGHISSEPHESERGIYVALASNTTRPGIINASPYALTYRASPLYSLYSEUVALPRO	420
DB	1201	AGACACAGTTTCTCTCTCGAGGTAAACGGGAAATGATATATGATPAAAAAGCTGTACCT	1260
QY	421	PROPHELYSPROGINVALTHMSEGLUTHRASPTHARGLYTRPHEASPGILUINPHETHR	440
DB	1261	CCTTTTAAACCTCAAGATACATCTGAGACGATCTCTGATATTTTGTATGAAATTTTACA	1320
QY	441	ALAGINTHRILETHRIETHRPROPROGLULYSTRYASPGIUSASPGIYMETASPCYMETEC	460
DB	1321	GCTCAGACTATTAACAATACACCACTGAAAAAATATGATGAGATGGATATGACTTCGATG	1380
QY	461	ASPANGIUAARGARPROHISAPHEPROGLINPHESERTYRSERIASERGIYARGILU	479
DB	1381	GACATATGAGAGGCGGCGGCAATTTCCCTCAATTTTCTTACTCTGCAGATGGACGAGAA	1437
RESULT 2			
ABLS50839			
ID	ABLS50839	standard; cDNA; 1440 BP.	
XX	AC	ABLS50839;	
XX	DT	20-JUN-2002 (first entry)	

DE Human Akt3 encoding cDNA SEQ ID NO:10.
 XX
 KW Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;
 KW apoptosis; serine/threonine kinase; heat shock protein; anticancer;
 KW cytoskeletal; cardiant; vasotrophic; hepatotropic; neuroprotective;
 KW antidiabetic; nootropic; cancer; diabetes; Alzheimer's disease;
 KW cell death; radiation; brain ischaemia; cardiac ischaemia; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..1440
 FT /*tag= a
 FT /product= "Akt3"
 XX
 PN WO200215925-A1.
 XX
 PD 28-FEB-2002.
 XX
 PD 22-AUG-2001; 2001WO-JP007179.
 XX
 PR 22-AUG-2000; 2000JP-00251529.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (TSURU/) TSURUO T.
 PI Tsuruo T, Fujita N, Sato S;
 XX
 DR WPI; 2002-292035/33.
 DR P-PDB; ABB06998.
 XX
 PT Regulation of apoptosis by promoting or inhibiting the intracellular
 binding of Akt with Hsp90, useful for prevention and treatment of
 apoptosis-regulation associated diseases including cancer.
 XX
 PS Disclosure; Page 87-89; 93pp; Japanese.
 XX
 CC The present invention describes the regulation of apoptosis, in which the
 intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a
 heat-shock protein) is promoted or inhibited. The present invention also
 describes: (1) isoforms of Akt and Hsp90, and their partial peptides
 including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA
 encoding Akt or Hsp90 or their partial peptides including the binding
 domain; (4) expression vectors containing the DNA; (5) host cells
 transformed by the vectors; (6) production of Akt or Hsp90 or their
 partial peptides including the binding domain by culture of the
 transformed cells; (7) screening compounds for their ability to modify
 intracellular Akt activity by contact with cells expressing Akt or Hsp90;
 and (8) drug compositions containing antibodies recognizing the binding
 domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and
 Hsp90 have cytoskeletal, cardiant, vasotrophic, hepatotropic, antidiabetic,
 neuroprotective and nootropic activities. Blockade of the binding of
 Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.
 CC Akt and Hsp90 can be used in the prevention and treatment of diseases
 with which apoptosis regulation is associated, including cancer (such as
 gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and
 prostate cancer), diabetes, Alzheimer's disease, cell death caused by
 radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The
 present sequence encodes human Akt3 which is used in the exemplification
 of the present invention
 CC
 XX
 SO Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.18e-258 Length: 1440
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-869-079B-3 (1-479) x ABL50839 (1-1440)

QY 1 MetSerAspValThrIleValIysGluGlyTPValGlnLysArgGlyGluIlyrIleLys 20
 DB 1 ATGAGCGATGTTACATCTGTGAAAGAGGTGGGTTCAAGAGGCGAATATATATATA 60
 QY 21 AsnTrpArgProArgTyrPheLeuLeuLysTrpAspGlySerPheIleGlyTyrLysGlu 40
 DB 61 ACTGAGGCGCAAGATACCTTCCTTTGAAAGACAGATGGCTCATCTTACAGATATATAAG 120
 QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
 DB 121 AAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATCCAG 180
 QY 61 LeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpTr 80
 DB 181 TTATATGAACAGAACAGACCAAGCCAAACATTTATATCATGATGTCCTCCAGTGGACT 240
 QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGlu 100
 DB 241 ACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGAAAGGAAATGACAGAA 300
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
 DB 301 GCTATCCAGGCTGTAGCAGACACTGCAGAGCAAGAGAGAGAAATGAATTGATGAT 360
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrpHis 140
 DB 361 CCAACTTCACAAATGATATATATAGAGAGAAAGATGATGCTCTACACCCATCAT 420
 QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
 DB 421 AAAGAAACACATGATGATATTTGACTATTTGAAACTGATGATAAAGCACTTTGGG 480
 QY 161 LysValIleLeuValArgGluLysLysAspGlyLysTyrTyrAlaMetLysIleLeuLys 180
 DB 481 AAAGTATTTTGGTTCGAGAGAAAGCAAGTGAATAATCTATGTAAGATTCGGAAG 540
 QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValIle 200
 DB 541 AAAGAAAGCATATATGCAAGAGATGAGGACACACTCTAATCTGAAGCAGAGATATTA 600
 QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 DB 601 AAGAACACATGACATCCCTTTTAAACATCTTGAATAATTCCTCCAGACAAAGACCG 660
 QY 221 LeuCysPheValMetGluTyrValAsnGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
 DB 661 TTGCTGTTTGTATGGAATATGATGAGGCGGAGCTGTTTTCATTTGTCAGAGAG 720
 QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGlnIleValSerAlaLeuAsp 260
 DB 721 CGGGTGTCTCTGAGGACCGCACAGCTTCTATGTCAGAAATGTCTCTGCTTGAC 780
 QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
 DB 781 TATCTACATCTCGGAAAGATGTGTACCTGATCTCAATTTGAGAAATTATATGCTGGAC 840
 QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
 DB 841 AAAGATGCGCACATAAATTAACATTTTGAACCTTGAAGAGGAGTCAACAGATGCA 900
 QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrTyrLeuAlaProGluValLeuGluAsp 320
 DB 901 GCCACCATAGACATCTGTGCGCACTCCAGAAATATCTGACACAGAGGTGTAGAAAGAT 960
 QY 321 AsnAspTyrGlyArgAlaValAspTrpTyrPheGlyLysValIleMetTyrGluMetCys 340
 DB 961 AATGATTAAGCGCGAGCACAATGATGATCGTGGCGCTTGAATGATATGATGATGATG 1020
 QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
 DB 1021 TGTGGAGGTTACCTTCTTACCAACGACGACATGAGAACTTTGAAATTAATTAATTAAG 1080
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380


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Db      311 GCTATCCAGGCTGTACAGACAGACTGCAGAGCCAAAGAGAGAAATGAATTGTAGT 370
QY      121 ProThrSerGlnIleAspAsnIleGluGluMetAspAlaSerThrHis 140
Db      371 CCACTTCACAAATATATATAGAGAGAGAAAGATGATGCTCTACAAACCCATCAT 430
QY      141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
Db      431 AAAAGAAACACATGATGATGATTTGACTATTGAAACCTAGTAAAGCACTTTTGAG 490
QY      161 LysValIleLeuValArgGlyLysValAspGlyLysTyrTyrAlaMetLysIleLeuLys 180
Db      491 AAAGTATATTTGGTTGGAGAGAGGCAATGGCAAAATCTATGCTGTGAAGATTCGAAG 550
QY      181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
Db      551 AAAAGAGCTATTTCCTCAAAAGATGAGAGTGGCACACACTCTAACTGAAAGCAGATATTA 610
QY      201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
Db      611 AAGAACACTAGACATCCCTTTTAAACATCCTTGAAATATTCCTCCAGCAAAAGACCGT 670
QY      221 LeuCysePheValMetGluTyrValaAsnGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
Db      671 TTGTGTTTTGTGTGATGGAATATGTATATGGGGGCGACCTGTTTTCCATTGTTCGAGAGAG 730
QY      241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGlnIleValSerAlaLeuAsp 260
Db      731 CCGGTGTTCTTCGAGAGCCGACACGCTTTCTATGTCGAAATTTCTCTGCTTGGAC 790
QY      261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
Db      791 TATCTACATTCGCGAAAGATTTGTGTACCGTATCTCAAGTTGAGATCTAATGCTGGAC 850
QY      281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCyseLysGlyGlyIleThrAspAla 300
Db      851 AAAGATGGCCACATAAATTAACAATTTGACCTTTGCAAAAGAGGATCAACAGTGA 910
QY      301 AlaThrMetLeuThrPheCyseGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db      911 GCCACCATTAAGACATTTCTGTGGCACTCCAGATATCTTGGCACCAAGGTGTTAGAGAT 970
QY      321 AsnAspTyrGlyArgAlaValAspTyrPyrGlyLeuGlyValaMetTyrGluMetMet 340
Db      971 AATGACTATGCGCGAGACAGTACGCTGTGGGGCTGAGGGGTGTATGATGAATGATG 1030
QY      341 CyseGlyArgLeuProPheTyrAsnGlnAspHisGlnLysLeuPheGluLeuIleLeuMet 360
Db      1031 TGTGGAGGTTACCTTTCTTACCAACGAGACCATGAGAAAACCTTTGAAATTAATTAAATG 1090
QY      361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
Db      1091 GAAAGACATTAATTTCTCGAACACTCTCTTCGATGCAAAATCATTTGCTTTCAGGGGCTC 1150
QY      381 LeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaLysGluIleMet 400
Db      1151 TTGATTAAGAGATCAATATAACCGCTTGGTGGAGGACCAAGATGATCAAAAGAAATTATG 1210
QY      401 ArgHisSerPhePheSerGlyValaAsnTyrPyrGlnAspValTyrAspLysLeuValPro 420
Db      1211 AAGACACAGTTTCTCTCTGAGTAAACCTGCAAGATGATATGATTAATAAAGCTTGTAACCT 1270
QY      421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
Db      1271 CCTTTAAACCTCAATACATCTGAGACAGATACATAGATTTTATATAGAAATTTTAA 1330
QY      441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
Db      1331 GCTCAGACTATTAACAATAACACCACTGAAAAATATGATGAGGATGATGATGATGATG 1390
QY      461 AspAsnGluArgArgProHisPhePheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
Db      1391 GACAAATGAGAGGCGCGCAATTCCTCAATTTTCTACTCTGCAAGTGGAGAGAA 1447

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RESULT 5
AAC61592
ID AAC61592 standard; DNA; 2367 BP.
XX
AC AAC61592;
XX
DT 19-FEB-2001 (first entry)
XX
DE DNA encoding a human kinase B-gamma polypeptide.
XX
KW Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;
KW phosphoinositide 3-kinase; insulin signalling;
KW pleckstrin homology domain; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 10..1449
FT /tag= a
FT /product= "kinase B-gamma polypeptide"
XX
XX MO200058446-A1.
XX
XX 05-OCT-2000.
XX
XX 23-MAR-2000; 2000W0-SE000571.
XX
XX 25-MAR-1999; 99SE-00001115.
XX
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX Altersand A;
XX
XX WPI: 2000-647230/62.
XX
XX P-PSDB: AAB19284.
XX
XX
XX Novel human protein kinase B gamma polynucleotides and polypeptides
XX PT useful as probe or primers in polymerase chain reaction and to raise
XX PT antibodies useful in diagnostic assays for detecting polypeptide
XX PT expression.
XX
XX PS Claim 1; Page 16-19; 27pp; English.
XX
XX
XX The present sequence encodes a human protein kinase B gamma (PKB)
XX CC polypeptide. PKB is activated by insulin or insulin growth factor 1.
XX CC lipid products of phosphoinositide 3-kinase act in insulin signalling by
XX CC binding to pleckstrin homology domains of PKB. PKB polynucleotides may be
XX CC used as a source of probes and primers. PKB polypeptides are used to
XX CC raise antibodies, which are used in diagnostic assays. The polypeptides
XX CC are also useful for screening for compounds which affect insulin
XX CC signalling pathways
XX
XX SQ Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,326-258 Length: 2367
XX Score: 2558.00 Matches: 479
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-869-079B-3 (1-479) x AAC61592 (1-2367)
XX
QY 1 MetSerAspValThrIleValLysGluGlyTyrPyrAlaGlnLysArgGlyLysTyrIleLys 20
Db 10 ATGAGCGAGTGTATACCATTTGTGAAGAAGGTTGCTTCAAGAAAGGAGAAATATATTA 69
QY 21 AsnTPArgProArgTyrThrLeuLeuLysThrAspGlySerPheIleGlyTyrTyrGlu 40
Db 70 AACTGAGGCGCAAGTACTTCTTTTGAAGACAGATGGCTCATTCATGAGATATAAGAG 129

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QY 41 LysProGlnAspValAspLeuProGlyProLeuAsnAspPheSerValAlaIysCysGln 60
 DB 130 AAACCTCAAGATGGATTTACTTATCCCTCAACAACCTTTTCATGGCGAATAATGCCAG 189
 QY 61 LeuMetLysThrGluArgProIysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
 DB 190 TTPATGAAACAGACGACCAAGCAACCAATTTATATCATGATGTCTCCAGTGGAGCT 249
 QY 81 ThrValIleGluIuArgThrPheHisValAspThrProGluGluArgGluTrpThrGlu 100
 DB 250 ACTGTTATAGAGAACATTTCATGTAGATATCCAGAGGAAAGGAAAGATGACAGAA 309
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluIuArgMetAsnCysSer 120
 DB 310 GCTATCAGGCTGTAGCAGACAGCTGCAGAGGCAAGAGAGAGATGAAATTTGTAAGT 369
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 140
 DB 370 CCMACTTCAAAATTTGATATATAGAGAGAGAGATGATGCTCTACAAACCATCAT 429
 QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
 DB 430 AAAGAAAGCAATGATGATTTTGTAGCTATTGAAACTACTAGTAAAGGCACCTTTGGG 489
 QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
 DB 490 AAGTTATTTTGGTTGAG 549
 QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
 DB 550 AAAGAAGTCATTTATCCAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 609
 QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 DB 610 AAGAACACTAGACATCCCTTTTACATCCTTGAATATTTCTTCCAGCAAAAGACCGT 669
 QY 221 LeuCysPheValMetGluTyrValAlaAsnGlyGlyLeuPhePheHisLeuSerArgGlu 240
 DB 670 TTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCATTTGTGAGAGAG 729
 QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
 DB 730 CGGGTGTCTCGAGAGACCGCACACGTTTCTATGGAGCAAAATTTGCTCTGCGCTGGAG 789
 QY 261 TyrLeuHisSerGlyLysIleValIlyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
 DB 790 TATCTACATTCGCGAAAGATTTGTGTACCGTGTACCTGAAGTTGAGAGATCTAAAGCTGAGAC 849
 QY 281 LysAspGlyHisIleLeuValIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
 DB 850 AAGAGATGCCACATTAATAATTCAGATTTTGGACCTTGCAGAAAGAGAGATCACAGATGCA 909
 QY 301 AlaThrMetLysThrPheCysGlyLysProGluTyrLeuAlaProGluValIleGluAsp 320
 DB 910 GCCACATGAGAGCATTTCTGTGCACTCCAGATATCTGGCACAGAGGTTTAAAGAT 969
 QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
 DB 970 AATGACTATAGCCGACAGACAGTACTGTGGGCGCTGAGGGGTTGTCTGATGTAAGAAATGATG 1029
 QY 341 CysGlyArgLeuProPheTyrAsnGlnAsnHisGluLysLeuPheGluLeuIleLeuMet 360
 DB 1030 TGTGGGAGGTTACCTTTCTACAAACGAGACCAAGAAACCTTTTGAATTAATTAATTAAG 1089
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
 DB 1090 GAAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTCAGGGGCTC 1149
 QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMet 400
 DB 1150 TTGATTAAGAGATCCAATTAACCCCTTGGTGAGAGACAGATGATCCAAGAAATTAATTAAG 1209
 QY 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420

DB 1210 AGACACAGTTTCTTCTCTGAGATGAACCTGCAGAGATATATATATAAAAGCTGTACCT 1269
 QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
 DB 1270 CTTTAAACCTCAAGTAAATCATCTGAGACAGATATATTTGATGAGAAATTTTACA 1329
 QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
 DB 1330 GCTCAGACTTATTAACAATTAACCACTGAAATTAAGATGATGATGATGATGATGATG 1389
 QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
 DB 1390 GACAAATGAGAGCGCGCCGATTTCCCTCAATTTTCTTACTCTGCAAGTGCAGAGAA 1446
 RESULT 6
 ID ADC26888 standard; DNA; 2811 BP.
 AC ADC26888;
 DT 18-DEC-2003 (first entry)
 XX
 DE DNA encoding human Akt3.
 KW de; gene; Akt; human; apoptosis; myocardial infarction;
 KW hyperproliferative disease; cancer; rheumatoid arthritis;
 KW inflammatory Bowel disease; osteoarthritis; leiomyoma; adenoma;
 KW haemangioma; fibroma; vascular occlusion; restenosis; atherosclerosis;
 KW pre-neoplastic lesion; adenomatous hyperplasia;
 KW prostatic intraepithelial neoplasia; carcinoma in situ;
 KW oral hairy leukoplakia; psoriasis.
 XX
 OS Homo sapiens.
 XX
 PN US200314204-A1.
 XX
 PD 31-UTL-2003.
 XX
 PF 19-DEC-2002; 2002US-00324985.
 XX
 PR 19-DEC-2001; 2001US-0342155P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Spencer D;
 XX
 DR WPI; 2003-720709/68.
 XX
 PT New expression vector for modulating apoptosis or for treating myocardial
 PT infarction or cancer, comprises an inducible chimeric protein that
 PT comprises a mutant Akt polypeptide fused to a ligand-binding domain.
 PS Disclosure; SEQ ID NO 4; 38pp; English.
 XX
 CC The invention relates to an expression vector comprising an inducible
 CC chimeric protein which comprises a mutant Akt polypeptide fused to a
 CC ligand-binding domain. The composition and methods are useful in
 CC modulating apoptosis or in treating myocardial infarction or
 CC hyperproliferative diseases such as cancer, rheumatoid arthritis,
 CC inflammatory bowel disease, osteoarthritis, leiomyoma, adenoma,
 CC lipoma, haemangioma, fibroma, vascular occlusion, restenosis,
 CC atherosclerosis, pre-neoplastic lesions (e.g. adenomatous hyperplasia or
 CC prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy
 CC leukoplakia or psoriasis. The present sequence represents DNA encoding
 CC human Akt3.
 XX
 SQ Sequence 2811 BP; 905 A; 506 C; 562 G; 818 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,93e-258 Length: 2811
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-869-079B-3 (1-479) x ADC26888 (1-2811)

QY 1 MetSerAspValThrIleValIysGluGlyTTPValGlnIleAspGlyIleuIleuMet 20
DB 1 ATGAGGAGTGTATCCATTGTGAAGAAGGTGGCTTCAGAAAGCGGGAGAAATATATATAA 60
QY 21 AsnTPArgProArgTyrPheLeuLeuIleuIleuIleuIleuIleuIleuIleuIleu 40
DB 61 AACTGAGGCGCAAGATACCTCTTTTGAAGACAGATGGCTCATCTTCAATGAGATATAAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValIleuIleuIleu 60
DB 121 AAACCTCAAGATGGATTTACCTTATCCCTCAACACTTTTCACTGGCAAAATGCCAG 180
QY 61 LeuMetIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 80
DB 181 TTATGATAAACAAGACGACCAAGCAACATTTATATGATGATGCTCCAGTGAAGT 240
QY 81 ThrValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 100
DB 241 ACTGTTATAGAGAACATTTTCATGTAGATCTCCAGAGAAAGGAGAAATGACAGAA 300
QY 101 AlaIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 120
DB 301 GCTATCAAGCTGTACAGACAGCTGCAGAGGCAAGAGAGAGAAATGAAATTTGAGT 360
QY 121 ProThrSerGlnIleuAspAsnIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
DB 361 CCAACTTCACAAATTGATATATATAGAGAGAGAAAGATGATGCTCTCAACCCATCAT 420
QY 141 LysAspGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 160
DB 421 AAAAGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
QY 161 LysValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 180
DB 481 AAAGTTATTTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 181 LysGluValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
DB 541 AAAGAGTCAATTATTCAGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 600
QY 201 LysAsnThrArgHisProPheLeuIleuIleuIleuIleuIleuIleuIleuIleu 220
DB 601 AAGAACACTAGACATCCCTTTTAAACATCTTGAAATATTTCCCTCCAGCAAAAGAC 660
QY 221 LeuCysPheValMetGluTyrValIleuIleuIleuIleuIleuIleuIleuIleu 240
DB 661 TTGTGTTTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyValAlaGluIleuIleuIleu 260
DB 721 CGGGTGTCTCTGAGAGACCGACACGTTCTATGAGCAAAATGCTCTGCTGAGAC 780
QY 261 TyrLeuHisSerGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 280
DB 781 TATCTACATTCGCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 281 LysAspGlyHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 300
DB 841 AAAGATGGCCACATAAAATTTACAGATTTTGAATTTGCAAAAGAGAGATCACAGATG 900
QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValIleuGlu 320
DB 901 GCACACATGAGACATTTCTGTGCACTCCAGAAATATCTGGACCAAGAGGTAAAGAA 960
QY 321 AsnAspTyrGlyArgAlaValAspTyrTyrGlyIleuGlyValIleuIleuIleu 340
DB 961 AATGACTATAGCGGAGACAGTACGTGTGGGGCTTAGGGGTGTGTATGTAATGATG 1020

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QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluIleuIleuIleuIleuIleuIleu 360
DB 1021 TGTGGAGGTTACCTTTCTTACACACAGACCATGAGAACTTTTGAATTAATTAATG 1080
QY 361 GluAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 380
DB 1081 GAAGACATTAATTTCTTCAACACCTCTTCAATGCAAAATCATTTGCTTCAAGGCTC 1140
QY 381 LeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 400
DB 1141 TTGATTAAGAGATCCAAATTAAGCCTGTGTGAGAGACCAAGATGACAAATAATG 1200
QY 401 ArgHisSerPhePheSerGlyValAlaAsnTPGlnAspValIleuIleuIleuIleu 420
DB 1201 AGACACAGTTCTTCTTCTGAGATTAACGCAAGATGATATGATTAAGAACTTTGACT 1260
QY 421 ProPheLysProGlnValIleuIleuIleuIleuIleuIleuIleuIleuIleu 440
DB 1261 CTTTTTAAACCTCAAGTAAACATCTGACACAGATCTAGATATTTGATGAGAAATTT 1320
QY 441 AlaGlnThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 460
DB 1321 GCTCAGACTATTACATTAACACACCTGAAATAATGATGAGATGATGAGACTGAC 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB 1381 GACATGAGAGGCGCGCGATTTCCCTCAATTTCTCTACTCTGCAAGTGAAGAGA 1437

RESULT 7
AD088265
ID AD088265 strand; DNA; 2811 BP.
XX
AC AD088265:
XX
DT 21-OCT-2004 (first entry)
XX
DE Human 14180 DNA encodes a rac gamma Ser/Thr protein kinase RAC-PK-gamma.
KW human; gene; de; cardiovascular disorder; thrombotic disorder;
KW differential expression; gene therapy; aberrant vascularisation;
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
KW dyslipidaemia; high blood pressure; heart failure; cardiac;
KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiac;
KW rac gamma Ser/Thr protein kinase; RAC-PK-gamma.
XX
OS Homo sapiens.
XX
PN WO2004063340-A2.
XX
PD 29-JUL-2004.
XX
PF 13-JAN-2004; 2004WO-US000393.
XX
XX
13-JAN-2003; 2003US-0439683P.
PR 05-FEB-2003; 2003US-0445216P.
PR 18-FEB-2003; 2003US-0448036P.
PR 12-MAR-2003; 2003US-0454189P.
PR 25-MAR-2003; 2003US-0457541P.
PR 29-APR-2003; 2003US-0466411P.
PR 08-MAY-2003; 2003US-0469041P.
PR 10-JUN-2003; 2003US-0477414P.
PR 13-JUN-2003; 2003US-0478560P.
PR 24-JUL-2003; 2003US-0489772P.
PR 28-JUL-2003; 2003US-0490660P.
PR 03-SEP-2003; 2003US-0499838P.
PR 22-SEP-2003; 2003US-0504786P.
PR 24-SEP-2003; 2003US-050570P.
PR 17-OCT-2003; 2003US-0512418P.
PR 27-OCT-2003; 2003US-0514660P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX

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PI Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;
PI Rogrigue-Way A, Tomlinson JE;
XX WPI; 2004-553729/53.
DR P-PSDB; ADQ88265.

XX Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.

XX Claim 1; SEQ ID NO 107; 512bp; English.

XX This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, which are differentially expressed in cardiovascular disease
CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiac, thrombotic, anticoagulant, antilipemic, hypotensive
CC and cardiac activities. This polynucleotide sequence is a human DNA
CC molecule that is differentially expressed in a patient with a
CC cardiovascular disorder, given in an exemplification of the invention.

XX Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,93e-258 Length: 2811
Score: 2558.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-869-079B-3 (1-479) x ADQ88265 (1-2811)

QY 1 MetSerAspValThrIleValIysGluGlyTTPValGlnIlyAsArgIyGluTyrIleIys 20
DB 1 ATGAGGATGTTTCCATTGGAAGAAAGTGGGTTCAAGAAAGGAGAAATATATATATATA 60
QY 21 AsnTTPArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrIlyGlu 40
DB 61 AACTGAGGCCAAGATACCTTCCTTTGAAAGACAGATGGCTCATTCATTCAGATATATAGAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaIysCysGln 60
DB 121 AAACCTCAAGATGGATTTTACCTTATCCCTCAACAACCTTTCAAGGGCAAAATGCCAG 180
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
DB 181 TTATATATAAACAAGAACCAAGCAACCAATTAATATATATATATATATATATATATATAT 240
QY 81 ThrValIleGluArgThrPheIleValAspThrProGluGluArgGluGluTyrPThrGlu 100
DB 241 ACTGTTATAGAGAAACATTTCTATGATATCTCCAGAGAAAGGAAAGATATGACAGAA 300
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluLysArgMetAsnCysSer 120
DB 301 GCTATCCAGGCTGTACAGACAGACTGACAGAGCAAGAGAGAGAGAAATGATTTGATG 360
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 140
DB 361 CCAACTTCACAAATTTGAT 420
QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160

DB 421 AAAAAGAAAGCAATGATGATTTTGACTATTGAAACTAGTAAAGCACTTTGGG 480
QY 161 LysValIleLeuValArgIleLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 481 AAAGTATATTTGGTTGGAGAGAAAGCAAGTGAAGAAATATATATATATATATATATATAT 540
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValIleu 200
DB 541 AAAGAACTCTTTTTCAGAAAGATGAGTGGACACACTTAACTAAAGCAAGATATTA 600
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 601 AAGAACATTAAGACATCCCTTTTAAACATCTTGAATATATCTCCACAGCAAAAGCCGT 660
QY 221 LeuCysPheValMetGluTyrValAlaAsnGlyGlyLysLeuPhePheHisLeuSerArgGlu 240
DB 661 TTGCTGTTTGTGTGATGAAATATGTTAATGGGGGGGACCTGTTTCCATTTGTCAGAGAG 720
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyValIleGluIleValSerAlaLeuAsp 260
DB 721 CGGATGTTCTTGAGGACCGCACAGTTCATGATGAGAAATGTCTCTGCTTGAC 780
QY 261 TyrLeuHisSerGlyLysIleValIlyArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 781 TATCTACATTCGGAAGAAATTTGTATCCGTGATCTCAAGTTGGAGAAATCAATGCTGGAC 840
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
DB 841 AAAGATGGCCACATTAATAATTCAGATTTTGGACTTTGCAAGAGGATCAACAGATGAC 900
QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 901 GCCACCATTAAGACATTCGTGGCACTCCAGAAATATCTGCACACAGAGGATGTAAGAAAT 960
QY 321 AsnAspTyrGlyArgAlaValAspTyrTyrPheGlyLeuGlyValAlaMetTyrGluMetC 340
DB 961 AATGATTAATGGCCGAGACATTAAGCTGTGGGGGCTTAAGGGGTTGATATATGAAATGATG 1020
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
DB 1021 TGTGGAGGTTTACCTTTCTTCAACACGACACATGAGAAACCTTTTGAATTAATTAATG 1080
QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1081 GAAGACATTAATTTCTCTGAACACTCTCTTCAGATGCAAAATCATTTGTCAGGGGCTC 1140
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyIlyProAspAspAlaLysGluIleMet 400
DB 1141 TTGATTAAGATCCAAATTAAGCCCTGTGTGAGAGACAGATGATCCAAAGAAATTAATG 1200
QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLeuValPro 420
DB 1201 AGACACAGTTCTTCTCTGAGTAACCTGGCAAGATGATATATGATTAATAAGCTTGACCT 1260
QY 421 ProPheLysProGlnValThrSerGluThrArgThrArgTyrPheAspGluGluPheThr 440
DB 1261 CTTTTTAAACCTCAAGATTAATCTTGAGACAGATCAATGATATTTGATTAAGATTTTAA 1320
QY 441 AlaGlnThrIleThrIlePheProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB 1321 GCTCAGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB 1381 GACAAATGAAGAGCGGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGAAGAGAA 1437
RESULT 8
AACT77341
ID AACT77341 standard; cDNA; 3285 BP.
XX
AC AAC77341;
XX
DT 08-FEB-2001 (first entry)

DB 1495 TGTGGAGGTTACTTTCTCAACACGAGACCACTGAGAACTTTTGAATTAATTTATG 1554

QY 361 GUAAPLLELYAPHPROAARGTHLEUSERSERAPALALYSERLEULEUSERGJLYLEU 380

DB 1555 GAAGACATTAATTTCTCTCGAACACTCTCTTCAGATGCAGAAATCATTTGCTTTCAGGGCTC 1614

QY 381 LEUILLLELYAPHPROAARGTHLEUSERSERAPALALYSERLEULEUSERGJLYLEU 400

DB 1615 TTGATTAAGATCCAAATTAACCGCTTGTGGAGGACCAATGATGTGCAAAAGAAATATG 1674

QY 401 ARGHISERHPHESERGIYVALASNTIPGLASPVATYRASPVLVLSLEVALPRO 420

DB 1675 AGACACAGTTTCTTCTCTGAGTAACTGGACAGATTAATGATTAATTAAGCTTTGACCT 1734

QY 421 PROPHELYAPROGINVALTHNSERGIUTHRASPTHARGTYRPHASERGJUGIUPHETHR 440

DB 1735 CCTTTTAACTCAAGTACATCTGACAGATFACATGATATTTTGTGATGAAGATTTACA 1794

QY 441 ALAGLTHRTLETHRTLETHRTPROPGIULYSTRASPGLUASPGJLYMEUSPGLVMEC 460

DB 1795 GCTCAGACTATTTCAATTAACACCACTGAAAAATATGATGAGATGGTATGAGCTGCATG 1854

QY 461 ASPASNGJUAARGRPROHISPHESERGIUPHESERTYRSEALASERGIVATSGLU 479

DB 1855 GACAAATAGAGGCGCGCCGCACTTTCCTCAATTTTCTTACTCTGCAAGTGCAGAGAA 1911

RESULT 9

AAA96637 standard; DNA; 1570 BP.

AC AAA96637;

AC XX 08-FEB-2001 (first entry)

DE DNA encoding a human Akt3 polypeptide.

KW Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1; hypoxia; apoptosis; necrosis; myocardial infarction; ischemia; reperfusion injury; myocardial ischemia reperfusion injury; stroke; liver damage; renal failure; organ transplantation; coronary artery; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 126..1523

FT /*tag= a

FT /product= "Akt3"

PN MO200056866-A2.

PD 28-SEP-2000.

XX 14-MAR-2000; 2000WO-US006574.

PF 19-MAR-1999; 99US-0125108P.

PR (AVET) AVENTIS PHARM PROD INC.

XX PA

XX PI Guo K, Pagnoni MF, Clark XL, Ivashchenko YD;

DR WPI, 2000-638260/61.

DR P-PSDB; AAB19011.

XX PT

XX Novel Akt3 nucleic acid and proteins capable of preventing apoptotic cell death induced by apoptosis stimulating kinase 1 useful for treating myocardial infarction or ischemia reperfusion injury.

XX PS Claim 3; Page 62-64; 73pp; English.

XX CC The present sequence encodes a human Akt3 protein. Expression of Akt3 prevents apoptotic cell death induced by apoptotic stimulating kinase 1 (ASK1). The Akt3 polypeptide is useful for inhibiting cell death.

CC preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or necrosis in a patient suffering from myocardial infarction or ischemia

CC reperfusion injury. The polypeptide is also useful for treating

CC myocardial infarction or ischemia reperfusion injury, where the

CC reperfusion injury is myocardial ischemia reperfusion injury or is

CC associated with stroke, liver damage, renal failure, organ

CC transplantation or coronary artery by pass grafting

XX

SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3,31e-242	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	3	Gaps:	1

US-09-869-079b-3 (1-479) x AAA96637 (1-1570)

QY 1 MetSerAPVALTHRTLEVALYSGIUGIYTPVALGILYARGLYGIUTYRIELLYS 20

DB 126 ATGAGCGATGTTTCCATTGTGAAGAAGTGGCTTCAGAGAAGGAGAGATATATAAAA 185

QY 21 AENTTPARGPROARGTYRPHLEULEULYSSTRASPGLSERPHEILEGIYTYRISGLU 40

DB 186 AACTGAGGCGCAAGATCTTCTTTGAAAGACGAAGGCTCATTCATAGGATATTAAGAG 245

QY 41 LVEPRGJLNASPVALASPLEUPROTYRPROLEUASNPSPHESERVALALALYSCYSGIN 60

DB 246 AANCTCAGATGTGATTTACTTATCCCTGAACACTTTTCAATGGCAAAATGCGAC 305

QY 61 LEUMELYSSTRGIULARGPROLYSPROAENTHRPHEILEIARGCYSEUGINTPTTHR 80

DB 306 TTAATGAAAAAGAAAGACCAAGCAACATTTATATATCATGATGCTCCAGTGGACT 365

QY 81 THRVALILEGLUARGTHRPHENISVALSPRTHPROGLUGLUARGIUGIUTPTNRGLU 100

DB 366 ACTGTTATAGAGAACATTTCTATGTAGATATCCAGAGAAAGGAAAGATGACAGAA 425

QY 101 ALAILEGLNALAVALAALASPARGLUENARGIUGIUGIUGIULARGMECAENYSSER 120

DB 426 GCTATCCAGGCTGTACAGACAGACTGCAAGGCAAGAGAGAGAGAAATTTAGT 485

QY 121 PROTHRSEGINLLEAPHANILEGIYGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGI 140

DB 486 CCAACTTCAAAATGATATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 545

QY 141 LVEARGLYETHMETENAPRPHASPTTYRLEULYLEULEUGIUYSGIYTHRPHGLY 160

DB 546 AAAAGAAAGCAATGATGATTTTGAATTTGAAACTATAGATTAAGGCACTTTGGG 605

QY 161 LVEVALILELEUVALARGIULYSALASERGIYLYSTRTYRAMELYSILEULYS 180

DB 606 AAGTTATTTTGGTTGAGAGAGGCAAGCAAAATATCTATGCTATGAAGATTCGAA 665

QY 181 LVEGLIUALILELALYASERGIUVALAHISTHLEUTHRGUSERATGVALL 200

DB 666 AAAGAAGTCAATTTGCAAGATGAGATGAGGACACACTTAAGTAAAGCAAGATTA 725

QY 201 LVEASNTHRARGHISPROPHLEUTHRSERLEULYTYRSEPHGLNTHLYSAPARG 220

DB 726 AAGAACATGACATCCCTTTTAAACATCTTGAAATATTTCTTCAGAAAGAACCGT 785

QY 221 LEUSPHEVALMETGIUTYVALAENGILYGIULYLEUPHRENIISLEUSERATGVALL 240

DB 786 TTGTGTTTGTGATGATATGTTATGAGGAGGAGACTGTTTTCATTTGTCGAGAG 845

QY 241 ARGVALPHESERGIULAPRGTHARGPHEUTYRGLYALGLIULYVALSERALALEUAP 260

DB 846 CGGATGTTCTGAGAGCGCACACGTTTCTATAGGCGAGAAATGTCCTGCTGGAGAC 905

QY 261 TYRLEHISERGIUYSLILEVALTYRARGDARLEULYLEULEULANLEUMELTLEUAP 280

DB 906 TATCTACATCCGAAAGATTGTGTACCGGATCTCAAGTTGAGATCTAATGCTGAGC 965
QY 281 LYSASPGYLHIHILEYSELLETHRRAPPHEGLYLEUCYELSGULGLYLETTRAPALA 300
DB 966 AAGATGGCCACATTAATAATTAACAGATTGTGACCTTTGCAAGAGAGATCAACAGATGCA 1025
QY 301 ALATHMETLYTHRPHECYSGLYTHRRPROGLUTYLLEUALPROGLUVALLEUGLUAP 320
DB 1026 GCCACCATGAAAGCATTTCTGTGCACTCCAGAAATATCTGGACCAAGGTGTTAGAAAT 1085
QY 321 AENASPTLYGLYARGALAVALAAPTPTPTGLYLEUGLYVALVAMETTYRGLUMET 340
DB 1086 AATGACTATAGCCGACAGACAGTACTGTGGGCGCTTGGAGGTTGTCAATGATGAATGATG 1145
QY 341 CYSGLYARGLEUPROTHETRYRANGINAPHEHIGLULYLEUPHEGLULEULEUMET 360
DB 1146 TGTGGAGGTTACCTTTCTACCAACGAGACATGAGAACTTTTGAATTTAAATTTAAAG 1205
QY 361 GLUASPTLLEYSPHEPROATGTTHLEUSERSERASPALALYSERLEUSERGLYLEU 380
DB 1206 GAAGACATTTAAATTTCTGCAACACTCTCTTCAGATGCCAAATCATTTGCTTACGGGCTC 1265
QY 381 LEULILEYASPPROASNYLSARGLEUGLYGLYPROASAPALAALYSGLULEUMET 400
DB 1266 TTGATTAAGATCCAAATAAACGCTTGTGGAGGACAGATGATGCCAAAGAAATTTAG 1325
QY 401 ARGHISERSPHEHESERGLYVALAENTTPGLINASPVALLTYRSPLYSLYSLVLEUVALPRO 420
DB 1326 AGACACAGATTTCTCTCTGAGTAACTGGCAAGATGTATATATAAAGCTTGTACCT 1385
QY 421 PROPHELYSPROGINVALTHRSERGLUTTHASPTTHARGTYRPHASPGULGIUPHETHR 440
DB 1386 CTTTAAACCTCAAGTACATCTGAGACAGATACACTATTTTGTATGAAGATTTTAC 1445
QY 441 ALAAGLTHRTLETHRTLETHRRPROFGLULYETLYRASPGLUASPGLYMETAPCY 459
DB 1446 GCTCAGACTATTAACAATAACACACACCTGAAATAATGTCAGCAATCA-----GATGT 1496
RESULT 10
AAH79025
ID AAH79025 standard; cDNA; 1570 BP.
XX AAH79025;
XX
DT 31-JAN-2002 (first entry)
XX
DE Human Akt3 encoding cDNA SEQ ID NO 1.
XX
DE Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;
KW cerebroprotective; neurotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;
KW osteopapthic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;
KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;
KW ischaemia reperfusion injury; stroke; organ transplantation;
KW coronary artery bypass; tumour cell survival; gene therapy;
KW Alzheimer's disease; osteoarthritis; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 126..1523
FT /tag= a
FT /product= "Akt3"
XX
XX PN MO200168850-A2.
XX
XX PD 20-SEP-2001.
XX
XX PF 09-MAR-2001; 2001MO-US007663.
XX
XX PR 14-MAR-2000; 2000US-00526043.
XX
XX PA (AVET) AVENTIS PHARM PROD INC.

XX
PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
XX
DR MPI, 2001-582452/65.
XX P-PSDB; AAG78018.
XX
PT New nucleic acid encoding human Akt3 protein, useful for inhibiting cell
PT death and treating myocardial infarction, ischemia reperfusion injury
PT associated with stroke, liver damage and renal failure.
XX
XX Claim 1, Page 59-62; 73pp; English.
XX
XX The invention relates to human Akt3 protein (AH/PH-domain containing
CC serine/threonine kinase, Akt) comprising a fully defined sequence
CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,
CC where the encoding polynucleotide hybridises under stringent conditions
CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570
CC base pairs defined in the specification. Akt3 has cerebroprotective,
CC neurotrophic, neuroprotective, antiarthritic, osteopapthic, vasotrophic and
CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis
CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a
CC regulatory region is useful for inhibiting cell death in cardiac myocytes
CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial
CC infarction or ischaemia reperfusion injury, particularly that associated
CC with stroke, liver damage, renal failure, organ transplantation or
CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving
CC Akt3 activity during treatment of patients suffering from myocardial
CC infarction or ischaemia reperfusion injury and inhibitors of Akt3
CC activity decrease tumour cell survival and result in tumour regression.
CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the
CC quantity of cell death and final infarct size, resulting in improved post
CC infarction function, improved quality of life and reduced mortality. In
CC patients with existing heart failure, gene therapy with Akt3 retards the
CC process of ventricular dilation and slows down disease progression. Akt3
CC gene therapy is useful for treating other disease states, involving cell
CC death by apoptosis, including Alzheimer's disease, liver degeneration or
CC osteoarthritis
XX
SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3,31e-242 Length: 1570
Score: 2402.00 Matches: 453
Percent Similarity: 98.91% Conservatve: 1
Best Local Similarity: 98.69% Mismatches: 3
Query Match: 93.90% Indels: 2
DB: 4 Gaps: 1
US-09-869-079B-3 (1-479) x AAH79025 (1-1570)
QY 1 MetSerAspValThrIleValysGluGlyTrpValGlnLysArgGlyGluTyrIleLys 20
DB 126 ATGAGGAGATTTACCAATGTGAAAGAGGTGGTTCCAAAGAGGGGAAATATATATAA 185
QY 21 AANTTPARPROARGTYRPHLEULEULYSTRASPGLYSERPHEILEGLYTRYRISGLU 40
DB 186 AACTGGAGGCCAAGATACCTCTTTTGAAGACAGATGCTCATTCATACAGATATAAAG 245
QY 41 LYSPPROGLINASPVALLTYRSPLYSLYSLVLEUVALPROGLUVALLEUGLUAP 60
DB 246 AAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGCCAAATGCCCAG 305
QY 61 LEUMETLYTHRGLUARGPROLYSPROAENTTPHEILLEIARGCYSEULGINTPTPTHR 80
DB 306 TTAATGAAACAGAACGACCAAGCAACACATTTATATACAGATGTCCAGTGAGACT 365
QY 81 ThrValIleGluArgThrPheHisValAAsPTTHRRPROGLUVALLEUGLUVALLEUGLU 100
DB 366 ACTGTTATGAGAGAACTTTATGATGATCTCCAGAGGAAAGGAAATGACAGAA 425
QY 101 ALAILEGALAVALAASPVALLTYRANGINAPHEHIGLULYLEUPHEGLULEULEUMET 120
DB 426 GCTATCCAGGCTGTGACAGACAGACTGCGAAGGCAAGAGAGAGATGATGTACT 485


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OY 121 ProthSerglnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
DB 486 CCACTTCACAAATTGATTAATATAGAGAGAGAGATGGCTCTACCAACCATCAT 545
OY 141 LysArgIleThrMetAsnAspPheAspTyrLeuIleuLeuGlyLysGlyThrPheGly 160
DB 546 AAAAGAAAGCAATGATGATTTTGACTATTGAAACTACTAGTAAAGCAGCTTTGGG 605
OY 161 LysValIleLeuValAlaGlyIleuLysSerGlyLysTyrTrpAlaMetLysIleLeu 180
DB 606 AAAGTTATTTGGTTCCAGAGAAAGGCAAGCAAAATACTATGCTATGAAATCTGAAG 665
OY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 666 AAAGAGCTCATTTATGCAAGAGATGAGTGGCACACCTCAACTGAAACAGAGATTTTA 725
OY 201 LysAsnThrArgHisPhePheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 726 AAGAACCTAGACATCCCTTTTAACTCCTTGAAATATTCCTTCCAGACAAAAGACCT 785
OY 221 LeuCysePheValMetGluTyrValAsnGlyGlyIleuLeuPhePheHisLeuSerArgGlu 240
DB 786 TTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTCCATTGTCGAGAGAG 845
OY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyValAlaGluIleValSerAlaLeuAsp 260
DB 846 CGGGGTGTTCTGTAGGAGCCGACACGTTTCTATGAGTCAAAATATGCTGCTGGAC 905
OY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 906 TATCTCATCTCCGAAAGATTTGTGTACCTGATCTCAAGTTGGAGATCTAAATGCTGGAC 965
OY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCyseGlyGlyIleThrAspAla 300
DB 966 AAAGATGGCCACATAAATTAACGATTTTGACCTTGCAAAAGAGGATCACAGATGCA 1025
OY 301 AlaThrMetLysThrPheCyseGlyThrProGluTyrLeuAlaProGluValIleuGluAsp 320
DB 1026 GCCACCATGAAAGCATTTCTGTGCACCTCCAGAAATATCTGGACACGAGGTGTAAGAAT 1085
OY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
DB 1086 AATGACTATGCGGAGAGAGTGTGTGGGCTTACGGGTTGTCTATGTAATGAATGATG 1145
OY 341 CyseGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
DB 1146 TGTGGGAGGTTACTCTTCTACAAACGAGGACCATGAGAAACTTTTGAATTAATTAATG 1205
OY 361 GluAspIleLysPheProAlaGlnThrLysSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1206 GAAAGACATTAATTTCTCTCAACACTCTCTTCAGATGCCAAATCATTTGACGGGCTC 1265
OY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400
DB 1266 TTATATAAGATCCAAATTAACCGCTTGAGAGAGACCAATGATGCAAAAGAAATTAATG 1325
OY 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
DB 1326 AGACACAGTTTCTCTCTGAGTAACCTGGCAAGATGTAATGTAATAAAAGCTTTGTAACCT 1385
OY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1386 CCTTTTAAACCTCAAGTAAATCATCTGAGACAGATACATGATTAATTTGATGAAGATTTACA 1445
OY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
DB 1446 GCTCAGACTATTACATTAACCACTGAAATAATGTGACGAATCA-----GATTGT 1496

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RESULT 11
AAA89264
ID AAA89264 standard; cDNA, 1570 BP.
XX

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AC AAA89264;
DT 28-MAR-2001 (first entry)
XX
DE Human serine/threonine protein kinase Akt3 cDNA.
KW Akt3; human; protein kinase; vascular endothelial growth factor; VEGF;
KW inducer; ischemia; cardiomyopathy; angiogenesis; tumour; gene therapy;
KM
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 126..1523
FT /tag= a
XX
PN MO200077190-A2.
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000MO-US015098.
XX
PR 11-JUN-1999; 99US-0138724P.
PR 03-NOV-1999; 99GB-00026058.
XX
PA (AVET ) AVENTIS PHARM PROD INC.
XX
XX Guo K, Ivashchenko Y, Clark K;
XX
XX WPI; 2001-025336/03.
XX
XX P-PSDB; AAB19996.
XX
PT Inducing expression of vascular endothelial growth factor, useful for
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal
PT ischemia or pulmonary ischemia, comprises administering a
PT serine/threonine protein kinase Akt protein.
XX
XX Example 1; Page 55-58; 67pp; English.
XX
XX The present sequence is that of cDNA coding for human Akt3 (see
XX AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase
XX capable of inducing vascular endothelial growth factor (VEGF) expression.
XX The sequence was deduced from 2 cDNA clones isolated from a human heart
XX cDNA library using a human Akt3 partial clone as probe. Akt3 is shorter
XX than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no
XX significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of
XX the molecules. A claimed method of inducing expression of VEGF in a cell
XX involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding
XX such a protein. The cell is preferably from a patient suffering from an
XX ischemic condition, especially cerebrovascular, renal, pulmonary, limb
XX or myocardial ischemia, or ischemic, idiopathic or hypertrophic
XX cardiomyopathy. The result is beneficial collateral blood vessel
XX formation. A claimed method of inhibiting angiogenesis in a patient
XX suffering from a tumour, comprises inhibiting the level of Akt activity
XX in the patient, thereby inhibiting production of VEGF. The method
XX comprises introducing an Akt antisense nucleic acid, an intracellular
XX binding protein (e.g. a scFv) that specifically binds the Akt protein, or
XX a nucleic acid encoding a dominant negative form of an Akt
XX
SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.:	3,31e-242	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	4	Gaps:	1

US-09-869-079B-3 (1-479) x AAA89264 (1-1570)

OY 1 MetSerAspValThrIleValLysGluGlyTTPValGlnLysArgGlyGluTyrIleLys 20
|||||

Db 126 ATGAGCATGTTACCATTTGTGAAGAAGGTTGGGTTCAAGAGAGGGAGAAATATATATAA 185
 QY 21 AANTPRARProArGthrPheLeuLeuYthrAspGlySerPheIleGlyTyrLeuVal 40
 Db 186 AACTGAGGCCAAGACTTCTTTTGAAGACAGATGGCTCATTTCACTAGAGATATATAAG 245
 QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
 Db 246 AAACCTCAAGATGTGATTTACTTATCTTATCCCTCAACACTTTTCAGTGGCAAAATCCAG 305
 QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnThr 80
 Db 306 TTAAAGAAAACAGAAAGACCAACCAACATTTATATACAGATGTCTCCAGTGGACT 365
 QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluThrGlu 100
 Db 366 ACTGTTATAGAGAACATTTCTATGTAGTATCTCCAGAGAGAAAGGAAAGATGACAGAA 425
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
 Db 426 GCTATCCAGCTGTAGACAGACTGCAGAGCAGAAAGAGAGAGATGAAATTTAGT 485
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
 Db 486 CCAACTTCACAAAATTGATATATAGAGAGAGAGATGATGCTCTCAACCCATCAT 545
 QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluLysGlyThrPheGly 160
 Db 546 AAAAGAAAGCAATGATGATTTTGTACTTTTGAACCTCTAGGTAAAGCACTTTGG 605
 QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
 Db 606 AAAGTATTTTGGTTGAGAGAGCAAGTGGAAATATCATGCTATGAAATTTGAA 665
 QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
 Db 666 AAAGAGTATATATGCAAGAGTGAAGTGGCACACACTCTAAAGCAAGAGATTA 725
 QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 Db 726 AAGAACACTAGACATCTCTTTTAAACATCTTGAAATATCTCTCCAGACAAAGACCT 785
 QY 221 LeuCysPheValMetGluTyrValAlaAsnGlyGluLeuPhePheHisLeuSerArgGlu 240
 Db 786 TTGTGTTTGTGATGGAATATGTTATGGGGGAGACTGTTTTCATTTGTGAGAGAG 845
 QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
 Db 846 CCGGTGTTCTTGAGAGACCGCACACGTTCTATGTGCAAGAAATTTGCTCTGCTTGAC 905
 QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
 Db 906 TATCTACATTCGGAGAAAGATTTGTATCGGTATCTCAAGTTGAGAAATCTTAATGCTGAC 965
 QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
 Db 966 AAAGATGGCCACATAAAATTACAGATTTTGACCTTTGCAAAAGAGATCAAGATGCA 1025
 QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
 Db 1026 GCCACCATAGAGCATTTCTGTGCACTCCAGAAATATCTGCAACCAAGGTTAGAGAGAT 1085
 QY 321 AsnAspTyrGlyArgAlaValAspTyrPheGlyLeuGlyValValMetTyrGluMetMet 340
 Db 1086 AATGACTATGGCCGAGAGATGACTGTGTGGGCTTGAGGGGTTTCATGATGAAATGATG 1145
 QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
 Db 1146 TGTGGAGGTTACTTTCTACACACAGACCATGAGAACTTTTGAATTAATTAATTAAG 1205
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
 Db 1206 GAAGACATTAATTTCTCTGAAACATCTCTTCAGATGCAAAATCATTTGCTTCAAGGCTC 1265

QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400
 Db 1266 TTGATTAAGGATCCAAATTAAGCCTTGTGTGAGAGACAGAGATGCAAAAGAAATTATG 1325
 QY 401 ArgHisSerPhePheSerGlyValAlaThrGlnAspValTyrAspLysLeuValPro 420
 Db 1326 AGACACAGTTTCTCTGTGAGTAACTGGCAAGATGATATGATATAAAAGCTTGACCT 1385
 QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
 Db 1386 CCTTTAAACCTCAAGTAACTGTGACAGACTAGTATTTTGATGAAAGAAATTTACA 1445
 QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
 Db 1446 GCTCAGACTATTAACATTAACACACTGAAAAATGTACAGATCA-----GATTGT 1496
 RESULT 12
 ADG85244
 ID ADG85244 standard; DNA; 1570 BP.
 XX
 AC ADG85244;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human Chrysoosporium associated DNA.
 XX
 KW ds; gene; beta-glucosidic bond; beta-xylosidic bond; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..1523
 FT /tag= a
 FT /product= "Chrysoosporium associated protein"
 XX
 PN US2004002136-A1.
 XX
 PD 01-JAN-2004.
 XX
 PF 21-MAR-2003; 2003US-00394568.
 XX
 PR 06-OCT-1998; 98WO-BP006496.
 PR 06-OCT-1999; 99WO-NL000618.
 PR 13-APR-2000; 2000US-00548938.
 XX
 PA (EMBL/) EMBL:ABR B. A.
 PA (BURL/) BURLINGAME R. P.
 PA (OLSO/) OLSON P. T.
 PA (SINI/) SINITSYN A. P.
 PA (PAR/) PARICHIE M.
 PA (BOUS/) BOUSSEON J. C.
 PA (PYNN/) PYNNONEN C. M.
 PA (PUNT/) PUNT P. J.
 PA (VZEL/) VAN ZEIJL C. M. J.
 XX
 PI Email:arb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parichie M;
 PI Bousson JC, Pynnönen CM, Punt PJ, Van Zeijl CMJ;
 DR WPI; 2004-061663/06.
 DR P-PSDB; ADG85245.
 XX
 PT Novel mutant Chrysoosporium strain comprising nucleic acid sequence
 PT encoding polypeptide of interest such as proteases and lipases, the
 PT nucleic acid sequence being operably linked to expression-regulating
 PT region.
 XX
 PS Disclosure; SEQ ID NO 1; 70pp; English.
 CC The invention relates to a mutant Chrysoosporium strain comprising a
 CC nucleic acid sequence encoding a polypeptide of interest. A mutant
 CC Chrysoosporium strain is useful for producing a polypeptide of interest by
 CC culturing a mutant Chrysoosporium strain under conditions permitting

expression of the protein or polypeptide, and recovering the subsequently produced polypeptide of interest. The conditions further permit secretion of the protein or polypeptide of interest. The polypeptides are useful for hydrolysing beta-glucosidic bonds. A polypeptide is useful for hydrolysing beta-xylosidic bonds. The present sequence represents human Chrysosporium associated DNA.

XX Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3..j1e-242	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	12	Gaps:	1

US-09-869-079B-3 (1-479) X ADG85244 (1-1570)

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QY 1 MetSerAspValThrIleValIySGluGlyTTPValGlnIyAspGlyGlyTyrIleIyS 20
DB 126 ATGAGCGATGTTACCAATGTGAAAGAGGTGGGTTCAAGAGGGGAGAAATATATATAA 185
QY 21 AsnTyrArgProArgTyrPheLeuLeuIySAspGlySerPheIleGlyTyrIySGlu 40
DB 186 AACTGAGGCCAAGATACCTTCCTTTGAGACAGATGGCTCATTCATAGATATAAGAG 245
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaIyS 60
DB 246 AAACCTCAAGATGGATTTACTTATCCCTCAACACTTTTCAAGGGCAAAATGCCAG 305
QY 61 LeuMetIySerThrIleuArgProIySProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
DB 306 TTATATATAACAAAGACCAAGCAACCAATTTATATACAGATGTCTCCAGTGGACT 365
QY 81 ThrValIleGluIyArgThrPheHisValAspThrProGluIyAspGluGlyTTPThrGlu 100
DB 366 ACTGTTATAGAGAACTTTCTCATGTAGATCTCCAGAGAAAGGAAAGATGACAGAA 425
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnIySGluGlyIyAspGlyIySAspCysSer 120
DB 426 GCTATCCAGGCTGTAGACAGACAGCTGCAGAGCAAGAGAGAGAAATGTAATGTAAT 485
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluIySAspGlyIySAspThrThrHis 140
DB 486 CCAACTTCACAAATTTGATATATATAGAGAGAGAGATGATCCCTTACACCCATCAT 545
QY 141 LysArgIySerThrMetAspPheAspTyrLeuIySLeuLeuGlyIySGlyTTPPheGly 160
DB 546 AAAGAAAGCAATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 605
QY 161 LysValIleLeuValIySGluIySAspGlyIySAspGlyIySAspGlyIySAspGly 180
DB 606 AAAGTATTTTGGTGTGAGAGAGAGCAAGTGAATAATCTATCTATGAAGATTTCTGAAG 665
QY 181 LysGluValIleIleAlaIySAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 666 AAAGAAGTCATTTTCACAAAGATGAGTGGCACACCTTAACTGAAGCAGAGATATTA 725
QY 201 LysAsnThrArgHisAspPheLeuThrSerLeuIySAspGlyIySAspGlyIySAsp 220
DB 726 AAAGAACTTAGACATCCCTTTTAAACCTTTTAAACCTTTTAAACCTTTTAAACCTTT 785
QY 221 LeuCysPheValMetGluTyrValIySGluIySAspGlyIySAspGlyIySAspGly 240
DB 786 TTGTGTTTGTGATGGAATGTGTTAATGGGGGAGCTGTTTTCATTTGTGAGAGAG 845
QY 241 ArgValIyPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB 846 CCGGTGTCTCTAGAGACCGCACACGTTTCTATGGGCGCAAAATTTGCTTGGCTTGGAC 905
QY 261 TyrLeuHisSerGlyIySValIySAspGlyIySAspGlyIySAspGlyIySAspGly 280

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DB 906 TATCTACATTCGCGAAAGATGTGTACCGGTGATCTCAAGTTGGAGAAATCTATGCTGAC 965
QY 281 LysAspGlyHisIleIySAspIleThrAspPheGlyLeuCysIySGluGlyIleThrAspAla 300
DB 966 AAAGATGGCCACATTAATAATTCAGATTTTGGACTTTGCAAGAAAGAGATCACAGATGCA 1025
QY 301 AlaThrMetIySerThrPheCysGlyThrProGluIyTyrLeuAlaProGluValLeuGluAsp 320
DB 1026 GCCACCATTAAGACATTCGTGTGACCTCCAGATATCTGGACACAGAGGTGTTAAGAT 1085
QY 321 AsnAspTyrGlyIySAspValAspTyrPyrGlyLeuGlyValIySAspGlyIySAspGly 340
DB 1086 AATGATTAAGCCGAGCAGATGATGCTGGGGCTGAGGGGTTGCTATGATGAATGATG 1145
QY 341 CysGlyIySAspLeuProPheTyrAsnGlnAspHisGluIySLeuPheGluLeuIleMet 360
DB 1146 TGTGGAGGTTACCTTTCTTACAAACGAGACCATGAGAACTTTTGAATTAATTAAG 1205
QY 361 GluAspIleIySAspPheProArgThrLeuSerSerAspAlaIySAspGlyIySAspGly 380
DB 1206 GAAGACATTAATTTCTCTGAACACTCTCTCAGATGCAAAATCATTTGCTTCAAGGCTC 1265
QY 381 LeuIleIySAspProAsnIySAspArgLeuGlyIySGlyIySAspAspAlaIySAspGly 400
DB 1266 TTGATTAAGATCCAAATTAAGCCCTGCTGAGAGACCGAGATGATCCAAAGAAATTAAG 1325
QY 401 ArgHisSerPhePheSerGlyIySAspTyrPyrGlnAspValIySAspIySLeuValPro 420
DB 1326 AGACACAGTTCCTCTCTGAGTAACTGGCAAGATGATATGATTAATAAGCTTGAACCT 1385
QY 421 ProPheIySAspProGlnValIySAspGlyIySAspThrArgTyrPheAspGlyIySAsp 440
DB 1386 CTTTAAACCTCAAGTAACTGAGACAGATTAAGTATTTGATTAAGATTAATTAAC 1445
QY 441 AlaGlnThrIleThrIleThrProProGluIySAspGlyIySAspGlyIySAspGly 460
DB 1446 GCTCAGACATTTACATTAACACCACTGAAATAATGTCAGCATCA-----GATTGT 1496

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RESULT 13
ADN71941
ID ADN71941 standard; cDNA; 2277 BP.
XX
AC ADN71941;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chicken serine/threonine protein kinase (akt1) encoding cDNA SEQ ID:27.
XX
KW kinase pathway inhibitor; anti-prostate cancer;
XX mitogen-activated protein kinase pathway inhibitor;
KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase pathway;
KW PI3K/Akt kinase pathway; cytoskeletal; MAP kinase inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
KW chicken; serine/threonine protein kinase; akt1; gene; ss.
XX
OS Gallus gallus.
XX
FH Key Location/Qualifiers
FT CDS 466..1398
FT /tag a
FT /product= "serine/threonine protein kinase (akt1)"
XX
PD MO2004041185-A2.
XX
XX 21-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034636.
XX PF
XX 31-OCT-2002; 2002US-0423340P.
XX PR
XX (UNRP) UNIV ROCHESTER.

XX Chang C, Lee Y, Lin W;
PI
XX
XX MPI: 2004-390508/36.
DR
DR P-PSDB; ADN71942.
XX
PT Composition useful in the treatment of e.g. prostate cancer comprises a
PT kinase pathway inhibitor and an anti-prostate cancer compound.
PS
PS Disclosure; SEQ ID NO 27; 118bp; English.
XX
XX The present invention describes a composition (C1) which comprises a
CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
CC Also described: (1) identification of a mitogen-activated protein (MAP)
CC kinase pathway inhibitor involving incubating an androgen or a
CC library of molecules with a cell containing an activable MAP kinase
CC pathway and selecting the molecules which inhibit the activation of the
CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
CC involving incubating a cell with hydroxyflutamide and potential
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway or
CC cytoskeletal activity, and can be used as a MAP kinase inhibitor,
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
CC prostate cancer inhibitor; and for reducing the number of prostate cancer
CC cells in a sample. The composition C1 provides effective combination
CC therapy as compared to prior therapies. The present sequence encodes
CC chicken serine/threonine protein kinase (akcl1), which is used in the
CC exemplification of the present invention.
XX
XX Sequence 2277 BP; 672 A; 490 C; 549 G; 566 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 3,95e-215 Length: 2277
Score: 2146.50 Matches: 404
Percent Similarity: 91.25% Conservative: 34
Best Local Similarity: 84.17% Mismatches: 37
Query Match: 83.91% Indels: 5
DB: 12 Gaps: 4
US-09-869-079b-3 (1-479) x ADN71941 (1-2277)
QY 1 MetSerAspValThrIleValysGluGlyTyrPValGlnLysArgGlyGluTyrIleLys 20
DB 466 ATGAATGAAGTGCAGTATGGAAGAGATGGCTCCACAAACGAGAGATATATCAAA 525
QY 21 AsnTParGProArgTyrPheIleuLeuLysGlySerPheIleGlyTyrIleGlu 40
DB 526 ACATGAGGCGACGATATTTCTTTTAAAGATGATGACATTCATTGGCTACAGGAA 585
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheserValAlaLysCys 59
DB 586 CGACCCCAAGACGTTACCAACGAGAAATCACTTAAATTAATCTTCAGTAGCTCGTGC 645
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79
DB 646 CAGCTATGAAGCACAAGACCTTAACCAACACATTTATCATTTAGATGCCCTCCAGTGG 705
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTyrPThr 99
DB 706 ACCACAGTATGTAAGAAACATTTCACTGAGACCTCCAGAGAGCGGAGAAATGAGACA 765
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluLysArgLysCys 119
DB 766 AAGCATATCCAACTTTGACACAGCTTCAAGAAACAGAGAAAGATGATGATTTT 825
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluGlnMetAspAlaSerThrThrHis 139
DB 826 AAGATCGTCTCTCTAGTATATTCAGGTGCTGAAGAAATGAAATTTCTATGACAAAG 885
QY 140 HisLysArgLys---ThrMetAsnAspPheAspTyrLeuLysLeuLysGlyTyr 158

DB 886 CCAAAACACAAAGTACCATGATGATTTGTAATCCTTAAGCTACCTGGGAAAAGGCACT 945
QY 159 PheGlyLysValIleLeuValArgLysLysAspGlyLysTyrTyrAlaMetLysIle 178
DB 946 TTTGGAAAGCTATTTTACTTAAAGAAAAGCAACCGACGGTATTTATCTATGAAAATT 1005
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
DB 1006 CTGAAGAAAGAAAGTATTGTAGCAAAAGATGAAATGACACACGCTGACAGAAACCGT 1065
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
DB 1066 GTTTTACCAAGACTCAGCGATCATCTTAAACAGCTTTAAAGTATCTTTCAGACACAC 1125
QY 219 AspArgLeuCysPheValMetGluTyrValaAsnGlyGluLeuPhePheHisSerSer 238
DB 1126 GATCGCTGTGTGTTTGTATGAGATGCTAAACGAGGGAGCTTTTTCATCTGTGCG 1185
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 1186 AAGAGACGCTGATTTTCTGAAGACCGGGCGCTTTTATGGGGCTGAGATTGTTCAAGC 1245
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 1246 CTGAGTTCCTGCAATTCAGAGAAAGATGGTGTACAGAGATTTGAAGCTGGAAATCTT 1305
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlyIle 297
DB 1306 ATGCTGGATTAAGACGGGCACTAAATTAATTCAGACTTTGACTATGTAAGAAAGCATTA 1365
QY 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
DB 1366 AAAAGATGAGCAACATGAAAGCTTCTGTGCACTCCAGAGTATCTTGACACAGAGGTG 1425
QY 318 LeuGluAspAsnAspTyrGlyArgAlaValaAspTyrPThrGlyLeuGlyValValMetLys 337
DB 1426 CTGGAGGATTAAGACATATGCTGTACAGTGTGCTGGTGGGATTTGAGATGTAT 1485
QY 338 GluMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
DB 1486 GAAATGATGTGTGGCGGCTCCCTTTCTTAATCAATCGACATGAAAGCTCTTTGAATC 1545
QY 358 IleLeuMetGluAspIleLysPheProArgThrIleSerSerAspAlaLysSerLeuLeu 377
DB 1546 ATCTTATGAGAAAGATGATGATTTCCAGCACTTGTCACTGAAGCAAAATCTCTCTTG 1605
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397
DB 1606 TCAGGTGTGCTTAAGAAAGATCTTAAGCAAAAGTTAGAGGGGATCTGATATGCCAAG 1665
QY 398 GluIleMetArgHisSerPhePheSerGlyValaAsnTPGlnAspValTyrAspLysLys 417
DB 1666 GAGATTTATGACACAAATTTCTTCTGCACTTGTGGCAAGATGATACGGGAAGAG 1725
QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 1726 CTGTATACCTCATTTAAGCACAAGTTACATCTGAAACAGATACAAAGATACCTTGATGA 1785
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1786 GAATTTTACAGCAACAGATGATTAACAATCACTCTCTGACCA-----GATACACGACATG 1839
QY 458 AspCysMetAspAsnGluArgArgProHisAspPheProGlnPheSerTyrSerAlaSerGly 477
DB 1840 GATGTGTAGCAATGAGAAAGACCTATTTCTCAGTTCTCTATTCACCGACGTGGA 1899
RESULT 14
AD085348
ID AD085348 standard; cDNA; 2593 BP.
XX
AC AD085348;
XX
DT 07-OCT-2004 (first entry)

XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #2162.
 XX human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;
 XX cancer; cell proliferative disorder; gene; ss.
 XX Homo sapiens.
 XX WO2004060270-A2.
 XX 22-JUL-2004.
 XX 15-OCT-2003; 2003WO-US029126.
 XX 18-OCT-2002; 2002US-0418988P.
 XX (GENT) GENENTECH INC.
 XX (MUTD) WU T D.
 XX (ZHOU) ZHOU Y.
 XX Wu TD, Zhou Y;
 XX WPI; 2004-534300/51.
 XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
 XX preventing or treating cell proliferative disorders such as cancer.
 XX Claim 1; SEQ ID NO 2162; 5504bp; English.
 XX The present invention describes an isolated tumour-associated antigenic
 XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 XX sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 XX (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 XX sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) -
 XX (c). Also described: (1) an expression vector comprising the above
 XX nucleic acid; (2) a host cell comprising the above expression vector; (3)
 XX a process for producing a polypeptide; (4) an isolated polypeptide
 XX comprising: (a) an amino acid sequence encoded by any of the above
 XX nucleotide sequences; (b) an amino acid sequence encoded by the full-
 XX length coding region of the above nucleotide sequences; or (c) a sequence
 XX having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 XX comprising the above polypeptide fused to a heterologous polypeptide; (6)
 XX an isolated antibody that binds to the above polypeptide; (7) a process
 XX for producing the antibody; (8) an isolated oligopeptide that binds to
 XX the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 XX binding organic molecule that binds to the above polypeptide; (10) a
 XX composition of matter comprising the above (chimeric) polypeptide,
 XX antibody, oligopeptide or TAT binding organic molecule, in combination
 XX with a carrier; (11) an article of manufacture comprising a container and
 XX the composition of matter contained within the container; (12) methods of
 XX inhibiting the growth of a cell that expresses the above protein, where
 XX the growth of the cell is at least in part dependent upon a growth
 XX potentiating effect of the above protein; (13) a method of
 XX therapeutically treating a mammal having a cancerous tumour comprising
 XX cells that express the above protein; (14) a method of determining the
 XX presence of a protein in a sample suspected of containing the protein
 XX described above; (15) methods of diagnosing the presence of a tumour in a
 XX mammal; (16) a method for treating or preventing a cell proliferative
 XX disorder associated with increased expression or activity of the above
 XX protein; and (17) a method of binding an antibody, oligopeptide or
 XX organic molecule to a cell that expresses the protein described above.
 XX The TAT sequences have cytosolic activities, and can be used in gene
 XX therapy. The composition and methods are useful for diagnosing,
 XX preventing or treating cancer. The composition is also used for preparing
 XX a medicament for the therapeutic treatment or diagnostic detection of a
 XX cell proliferative disorder or cancer. The present sequence represents a
 XX human TAT cDNA sequence from the present invention.
 XX SQ Sequence 2553 BP; 530 A; 747 C; 778 G; 538 T; 0 U; 0 Other;

Alignment Scores: 9.63e-211 Length: 2593
 Pred. No.: 2105.50 Matches: 397
 Score:

Percent Similarity: 90.21% Conservative: 36
 Best Local Similarity: 82.71% Mismatches: 42
 Query Match: 82.31% Indels: 5
 DB: 13 Gaps: 4
 US-09-869-079B-3 (1-479) x ADQ85348 (1-2593)
 QY 1 MetSerAspValThrIleValysGluGlyTPValGlnIleArgGlyGluTyrIleIys 20
 DB 181 ATGAGGACGCTGCTTGTGTGAAGAGGGTGGCTGCACAAAGAGGAGTACATCAAG 240
 QY 21 AsnTPArgProArgTyrPheLeuLeuIleValAspGlySerPheIleGlyTyrIleGlu 40
 DB 241 ACCGCGCGCCACGCTACTTCTCTCCCAAGAAATGATGACCTTCTTGGCTCAAGAG 300
 QY 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaIysCys 59
 DB 301 CGCGCCGACGATGTGGACCAAGCGTAGGCTCCCTCAACACTTCTGTGGCGCAGTGC 360
 QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79
 DB 361 CAGCTGATGAAAGCGAGCGGCCCGCCCAACACCTTCATCATCTGCTGCTGCAGTGG 420
 QY 80 ThrValIleGlnValArgThrPheHisValAspThrProGluGluArgGluTyrPThr 99
 DB 421 ACCACTGTATGAAACGCACTTCCATGTGAGACTCTTGAGAGCGCGAGAGTGTGAC 480
 QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCys 119
 DB 481 ACCGCCATCAAGACTGTGGCTGACGCGCTCAAGAAACAGAGGAGAGATGACTTC 540
 QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
 DB 541 CGGTGGGCTCAACCCAGTACAACTCAGGGCTGAAAGATGAGATGGTCCCTGGCCAA 600
 QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuIleLeuGluGlyLysGlyTyr 158
 DB 601 CCCAACACCGCTGACCTGACCTGAAACAGATTGAGTACTTGAAGCTCTGGGCAAGGCACT 660
 QY 159 PheGlyLysValIleLeuValArgIuValAspGlyLysPheTyrIleValMetLysIle 178
 DB 661 TTGGCAAGGTATCTGTGTGAAGGAGGACAGCGCCGCTACTACCACTGAAGATC 720
 QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
 DB 721 CTCACAAAGAAAGTCACTCTGGCCAGGACGAGGTGGCCACACATCCAGCAACCC 780
 QY 199 ValLeuLysAsnThrArgHisAspProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
 DB 781 GTCTTCAGAACTCCAGGACCCCTTCTCAACAGCCTTAAGTACTCTTCCAGACCCAC 840
 QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyGlyLysLeuPheHisLeuSer 238
 DB 841 GACCGCTCTGCTTGTGTGATGAGTACGCCAACGGGGGCGAGCTGTCTTCCACCTGTC 900
 QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyValAspIleValSerAla 258
 DB 901 CGGAAACGCTGTCTCCAGGACCGCGGCCCTCTTAAGGCGCTGAATTGTGTAGCC 960
 QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGlnLeu 277
 DB 961 CTGATTAATCTGCACTCGAGAAAGAACGTTGTATCCGGGACCTCAAGCTGAGAACTC 1020
 QY 278 MetLeuAspLysAspGlyLysIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
 DB 1021 ATGCTGACAAAGACCGGACATTAAGATCAAGACTTGGGCTGTGCAAGAGGGGATC 1080
 QY 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
 DB 1081 AAGGACGGTGCACCACTGAAGACCTTTTGGCAGACCTGAGATCACTGGCCCCCGAGGTG 1140
 QY 318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGluValValMetTyr 337

Db 1141 CTGAGACAAATGACTACGCGCTGACATGACCTGTGGGGGCTGGTGCATGTAC 1200

QY 338 GJUMETMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlnUlyLeuPheGluLeu 357

Db 1201 GAGATGATGAGCGCTGCTGCTTCTCAACCAAGACCAATGAGCTTTTGTAGCTC 1260

QY 358 ILeuMetGlnAspIleLeuPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377

Db 1261 ATCTCATGAGAGATCCGCTTCCGCGCAGCTTGTCGCCGAGGCCAAGTCTTGCTT 1320

QY 378 SerGlyLeuLeuIleUlyAspProAsnUlyAspLeuGlyGlyProAspAspAlaLys 397

Db 1321 TCAAGGCTCTCAAGAGAGACCCCAAGCAGAGCTTGCGGGGCTCCAGGACGCCAAG 1380

QY 398 GJUMETMetArgHisSerPhePheSerGlyValAsnThrGlnAspValTyrAspLysLys 417

Db 1381 GAGATATGATGATGATGCTTCTTGCGGATGCTGTGGAGACCTGTACGAGAAAGAG 1440

QY 418 LeuValProProPheLeuProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437

Db 1441 CTCAGCCCACTTCAAGCCCAAGCGTCAAGTGGAGACCTGACCAAGGATTTTGTAG 1500

QY 438 GJUMETMetAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457

Db 1501 GAGTTCACGCGCCAGATGATCAACCAACACCACTGACCAA-----GATGACAGCATG 1554

QY 458 AspCysMetAspAsnGlnArgArgProHisAspPheProGlnPheSerTyrSerAlaSerGly 477

Db 1555 GAGTGTGTGACAGCAAGCGCAGCGCCCACTTCCCAAGTTCCTTACTTGCGCCAGCGAC 1614

RESULT 15

ACD44893

ID ACD44893 standard; cDNA; 2978 BP.

AC ACD44893;

DT 10-SEP-2003 (first entry)

XX Human signal transduction pathway component HJBCX80 cDNA.

DE Human; signal transduction pathway component; gene; ss; gene therapy; human disorder; immune system disorder; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; muscular disorder; sinusitis; respiratory disease; nasal vestibulitis; nasal polyp; pulmonary disorder; cardiovascular disorder; congenital heart defect; Epstein's anomaly; hypoplastic left heart syndrome; renal disorder; acute kidney failure; end-stage renal disease; hyperproliferative disorder; Hodgkin's disease; leukemia; inflammatory disease; septic shock; bursitis; appendicitis; allergy; asthma; blood related disorder; thrombosis; atherosclerosis; myocardial infarction; endocrine disorder; Addison's disease; dysphagia; corticosteroid deficiency; reproductive system disorder; dysmenorrhea; testicular atrophy; gastrointestinal disorder; irritable bowel syndrome; infectious disease; cancer; wound healing; epithelial cell proliferation.

OS Homo sapiens;

XX US2003036505-A1.

PN 20-FEB-2003.

PD 20-SEP-2001; 2001US-00955999.

PF 25-SEP-2000; 2000US-0234997P.

PR (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Ni J, Ruben SM, Rosen CA, Young PE, Rohrschneider LR;

PI MPI: 2003-492122/46.

DR P-PSDB; ABO27207.

XX New isolated nucleic acids encoding signal transduction pathway component PT polypeptides, useful for diagnosing, treating, and/or preventing

PT disorders, such as cancer, infections, cardiovascular and inflammatory PT diseases.

XX Claim 3; Page 224-226; 297pp; English.

PS The invention relates to an isolated nucleic acid molecule. The methods CC and compositions of the present invention are useful for diagnosing, CC treating, preventing and/or prognosing disorders related to the novel CC polypeptides, such as neural disorders, immune system disorders (e.g. CC systemic lupus erythematosus, rheumatoid arthritis, or multiple CC sclerosis), muscular disorders, respiratory diseases (e.g. nasal CC vestibulitis, nasal polyps, or sinusitis), reproductive disorders, CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders CC (e.g. congenital heart defects, Epstein's anomaly or hypoplastic left CC heart syndrome), renal disorders (e.g. acute kidney failure, or end-stage CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease or CC leukemia), inflammatory diseases (e.g. septic shock, bursitis, or CC appendicitis), allergic reactions and conditions (e.g. asthma), blood CC related disorders (e.g. thrombosis, atherosclerosis or myocardial CC infarction), endocrine disorders (e.g. Addison's disease or CC corticosteroid deficiency), reproductive system disorders (e.g. CC testicular atrophy or dysmenorrhea), gastrointestinal disorders (e.g. CC dysphagia or irritable bowel syndrome), infectious diseases, and/or CC cancerous diseases. The polynucleotides can also be used to aid wound CC healing and epithelial cell proliferation. The present sequence CC represents a human signal transduction pathway component cDNA XX

SEQ Sequence 2978 BP; 613 A; 842 C; 889 G; 627 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:
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Percent Similarity:		90.21%	36
Best Local Similarity:		82.71%	42
Query Match:		82.31%	5
DB:		Gaps:	4

US-09-869-079B-3 (1-479) x ACD44893 (1-2978)

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QY 21 AsnTPArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrIyGln 40

Db 551 ACTCGCGCGCACGCTACTCTCTCTCAAGATGATGACCTTCAATGGCTACCAAGAG 610

QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59

Db 611 CGCGCGCAGAGATGTGACCAACGTAGAGCTCCCTCAACAACTTCTGTGCGCAGTGC 670

QY 60 GlnUlyMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79

Db 671 CAGCTGATGAAACGAGAGCGGCCCGCCCAACCTTCATATCCGCTGCTGCAGTGG 730

QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTyrThr 99

Db 731 ACCACTGTATGAAAGCACTTCCATGTGAGATCTCTGAGAGACGGAGAGTGGACA 790

QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCys 119

Db 791 ACCGCCATCAAGATGTGGCTGACGCGCTCAAGAGAGAGAGAGATGACCTTC 850

QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139

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QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluLysGlyThr 158

Db 911 CCCAAGACCGCGTGAACATGAACAGATTGATGACTTGAACCTGCTGGGCAAGGCACT 970

QY 159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrIleLysMetLysIle 178

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Qy 179 LeuLeuLeuLeuValIleIleIleAlaLeuAspGluValAlaIleThrLeuThrGluSerArg 198
Db 1031 CTCAGAGAGAGATGATCGGGCCAGAGAGAGGTGGCCACACTACACCGAGAACCGC 1090
Qy 199 ValLeuLeuAsnThrArgHisProPheLeuThrSerLeuLeuThrSerPheGlnThrLys 218
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Qy 219 AspArgLeuCysPheValMetGluTyValAsnGlyGluLeuPhePheHisLeuSer 238
Db 1151 GACCGCCTCTGCTTTGTCATGAGTACGCCACGGGGCGAGGTGTTCTTCCACTGTCC 1210
Qy 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrglValagluIleValSerAla 258
Db 1211 CCGGAGCGTGTGTTCTCCGAGACCGGGCCCGCTTCTATGCGGTGATTTGTCTCAGCC 1270
Qy 259 LeuAspTyrlleuHisSerGlyLys---IleValTyrrArgAspLeuLysLeuAsnLeu 277
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Qy 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
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Qy 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluTyrlleuAlaProGluVal 317
Db 1391 AAGGACGCTGCCACATGAAGACCTTTTGGCGACACTGATGACCTGCGCCCGAGGTG 1450
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Db 1451 CTGAGAGCAATGACTACGGCCGTGACGTGACTGGTGGGGGCTGGGCGTGTGATGTAC 1510
Qy 338 GluMetMetCysglYArgLeuProPheTyrrAsnGlnAspHisglulYsLeuPheGluLeu 357
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Qy 378 SerGlyLeuLeuLeuLeuLeuAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397
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Qy 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrrAspLysLys 417
Db 1691 GAGATCATGACGATCGCTTCTTGGCCGATCGTGTGGCAGCAGGTGACGAGAGAG 1750
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Db 1751 CTCAGGCCACCTTCAAGCCCGCAGGTCACTGCGAGCTGACACCAAGTATTTTGATGAG 1810
Qy 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrrAspGluAspGlyMet 457
Db 1811 GAGTTCACGGCCCAAGATGATCAACATCAACACCTGACCA-----GATGACAGCATG 1864
Qy 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrrSerAlaSerGly 477
Db 1865 GAGTGTGTGACAGCGAGCGCAAGCCCACTTCCCAAGTTCTTACTGGGCCAGCGGC 1924

Search completed: April 13, 2005, 09:07:38
Job time : 675 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 13, 2005, 07:36:25 ; Search time 236 Seconds
(without alignments)
3321.087 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558
Sequence: 1 MSQVTVKSGWVGKRGSEYK.....MNERPPHPQPSYSASGR 479Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2558	100.0	1547	US-09-851-670-1	Sequence 1, App11
2	2100.5	82.1	2626	US-09-590-740-5	Sequence 5, App11
3	2099.5	82.1	2181	US-09-417-197-70	Sequence 138, App1
4	2099.5	82.1	2184	US-09-417-197-138	Sequence 1, App11
5	2099.5	82.1	2610	US-09-212-771-1	Sequence 1, App11
6	2099.5	82.1	2610	US-09-031-058-1	Sequence 1206, App
7	2099.5	82.1	2610	US-09-023-655-1206	Sequence 1, App11
8	2099.5	82.1	2610	US-09-590-740-1	Sequence 1, App11
9	2004	78.3	1599	US-09-256-465-1	Sequence 1, App11
10	2004	78.3	1599	US-09-167-322-3	Sequence 3, App11
11	2004	78.3	1599	US-09-023-655-1004	Sequence 1004, App
12	1798.5	70.3	1254	US-09-590-740-3	Sequence 3, App11

13	916	35.8	1338	US-10-067-977-1	Sequence 1, App11
14	909	35.5	2370	US-09-031-295-1	Sequence 1, App11
15	905	35.4	2311	US-08-712-709-6	Sequence 6, App11
16	905	35.4	2311	US-09-111-444-6	Sequence 6, App11
17	905	35.4	2311	US-09-541-228-6	Sequence 72, App1
18	905	35.4	2311	US-09-016-434-772	Sequence 1676, App
19	872	34.1	2239	US-09-949-016-1676	Sequence 1, App11
20	865	33.8	2274	US-09-772-647-3	Sequence 1735, App
21	849	33.2	2336	US-09-949-016-1735	Sequence 1, App11
22	838	32.8	2599	5266464-1	Patent No. 5266464
23	838	32.8	2599	5266464-1	Patent No. 5266464
24	834.5	32.6	3321	US-09-023-655-1361	Sequence 1361, App
25	832	32.5	2374	US-09-190-9768-6	Sequence 6, App1
26	829	32.4	2245	US-09-225-749-24	Sequence 24, App1
27	823.5	32.2	2196	US-08-313-274-1	Sequence 1, App11
28	823.5	32.2	2262	US-09-949-016-5805	Sequence 5805, App
29	821.5	32.1	2751	US-09-417-197-72	Sequence 72, App1
30	819.5	32.0	3255	US-09-016-434-1471	Sequence 1471, App
31	819.5	32.0	6102	US-09-949-016-2007	Sequence 2007, App
32	807	31.5	2127	US-09-270-767-13509	Sequence 13509, App
33	807	31.5	2244	US-09-094-714A-48	Sequence 48, App1
34	798.5	31.2	2968	US-08-685-852-1	Sequence 1, App11
35	796	31.1	2705	US-09-949-016-839	Sequence 839, App
36	796	31.1	2715	US-09-949-016-1959	Sequence 1433, App
37	791.5	30.9	1636	US-09-016-434-1433	Sequence 1475, App
38	789.5	30.9	2506	US-09-949-016-1475	Sequence 3, App11
39	786	30.7	2754	US-09-429-322-3	Sequence 2099, App
40	781.5	30.6	2088	US-09-949-016-2099	Sequence 1, App11
41	781.5	30.6	2146	US-09-842-307-1	Sequence 1362, App
42	781.5	30.6	2146	US-09-023-655-1362	Sequence 52, App1
43	781.5	30.6	2201	US-09-566-921-52	Sequence 5749, App
44	769.5	30.1	1413	US-09-248-796A-4379	Sequence 4379, App
45	766.5	30.0	2499	US-09-949-016-5704	Sequence 5704, App

ALIGNMENTS

RESULT 1
US-09-851-670-1
; Sequence 1, Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699, 002/200130, 520
; CURRENT APPLICATION NUMBER: US/09/851, 670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1

Alignment Scores:
Pred. No.: 4.47e-290
Score: 2558.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 4
DB: 4
Gaps: 0

US-09-869-079B-3 (1-479) x US-09-851-670-1 (1-1547)

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QY 61 LeuMetLysThrGluArgProLysProAsnThrPheLeileArgCysLeuGlnTrpThr 80
DB 191 TTAATGAAACAGAACGACCAAGCCAAACACATTTATATATGATGTCCTCAGTGACT 250
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DB 251 ACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGAAAGGAAATAAGACAGAA 310
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCysSer 120
DB 311 GGTATCCAGGCTGTACAGACAGACTGCAGAGCCAAAGAGAGAGAAATGAAATTTGAT 370
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 140
DB 371 CCAACTTCACAATTTGATATATATAGAGAGAAAGATGAGATGCTCTCAACACCATCAT 430
QY 141 LysArgLysThrMetLysAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
DB 431 AAAAGAAACAAATGATATATTTGACTATTTGAAACTAGTAAAGCACTTTTGGG 490
QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 491 AAAGTATTTTGGTTGAGAGAAAGCAAGTGAATACTATGCTATGAAATTCGAAAG 550
QY 181 LysGluValIleLeuAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 551 AAAGAGTCAATTTATGCAAAAGATGAAAGTGGCACACCTCACTAAAGCAAGATTTA 610
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 611 AAGAACACTAGACATCTCTTTTAAACATCTTGAATATTTCTTCAGCAAAAGACCGT 670
QY 221 LeuCysPheValMetGluTyrValAlaGlyLysGluLeuPheHisLeuSerArgGlu 240
DB 671 TTGTGTTTGTGATGGAATGTGTAATGGGGGAGCTGTTTTCATTTGTGAGAGAG 730
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DB 731 CCGGTGTTCTGAGAGACCGCACACGTTCTATGAGGAGAAATGTCTCTGCTGGAGAC 790
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 791 TATCTACATTCGGAAGATGTGTACCGGTGATCTCAAGTTGAGATCTTAATGCTGAGAC 850
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
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QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuLeuMet 360
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QY 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLeuValPro 420
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QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1271 CTTTTTAAACCTCAAGTAAATCTGAGACAGATACATGATATTTGATGAAATAATTCA 1330
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
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QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB 1391 GACATGAGAGGCGCGCGATTTCCCTCAATTTCTCTACTCTGCAAGTGAAGAGAA 1447

RESULT 2
US-09-590-740-5
; Sequence 5, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-590-740-5

Alignment Scores:
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Score: 2100.50 Matches: 396
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Best Local Similarity: 82.50% Mismatches: 43
Query Match: 82.11% Indels: 5
DB: 4 Gaps: 4

US-09-869-079B-3 (1-479) x US-09-590-740-5 (1-2626)

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QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 344 ACCTGCGGCGCACGCTACTCTCTCTCAAGAACATGAGACCTTTATTTGGCTACAAAGAA 403
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheserValAlaLysCys 59
DB 404 CCGCTCAGAGATGTGATGATGAGAGAGATGCCACCTCAACAACTTCTCAGTGGCACAATGC 463
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleArgCysLeuGlnTrp 79
DB 464 CAGCTGATGAGACAGAGCGGCCCAACACCTTATATCATCCGCTGCTGAGATGG 523
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThr 99
DB 524 ACCAAGTCAATTGACGCACTTCCATGTGGAAAGCCCTGAGAGACGGGAAAGATGGGCC 583
QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCys 119
DB 584 ACCGCATTCAGACCTGTGGCCCATGAGCTCAAGAGGAGAGAGAGACATGAGACTTC 643
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
DB 644 CGATCAGGCTCACCCAGTGAACAATCAGGGGCTGAAGAGATGAGATGATGCTGCGCAAG 703

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159 TTTGGGAAGAGTATTTCTGTGAAAGAAAGGCCACAGGCCCTTACTATGCAATGATC 823
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Oy 179 LeuLyLyGlyValIleIleAlaLyvAspGlyValAlaIleThrLeuThrGlySerArg 198
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Oy 338 GlyMetMetCyvGlyArgLeuProPheTyrAsnGlnAspHisGlyLyvLeuPheGlyIleu 357
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Oy 398 GlyIleMetArgHiserPhePheSerGlyValAsnTyrGlnAspValTyrAspLyvLy 417
Db 1484 GAGATCAATGAGACACCGGCTCTTTGGCCAACATCGTGTGGCAGATGTGTATGAAAGAG 1543
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Oy 438 GlyPheThrAlaGlnThrIleThrIleThrProProGlyLyvTyrAspGlyAspGlyMet 457
Db 1604 GAGTTCAAGCTCAATATATCACTCAACGCCGCGCTGATCA-----GATGACAGCATG 1657
Oy 458 AspCyvMetAspAsnGlyArgArgProHisPheProGlnPheSerTyrSerAlaSerGly 477
Db 1658 GAGTGTGTGACAGTGAAGCGGAGGCGCACTTCCCAAGTTCTCTTACTCAGCCAGTGGC 1717

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: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP, et al.
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relati
: TITLE OF INVENTION: On A Cellular Response
: FILE REFERENCE: 3759-0110P
: CURRENT APPLICATION NUMBER: US/09/417,197
: CURRENT FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 70
: LENGTH: 2181
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: PKB-EGFP fusion
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(2178)
US-09-417-197-70

Alignment Scores:
Pred. No.:          5,1e-236          Length:          2181
Score:              2099.50           Matches:           396
Percent Similarity: 90.19%            Mismatches:        36
Best Local Similarity: 82.67%          Indels:            5
Query Match:        82.08%             Gaps:              4
DB:                  4

US-09-869-079B-3 (1-479) x US-09-417-197-70 (1-2181)

QY      1 MetSerAspValThrIleValIleGluGlyTyrValGlnIlybArgGlyGlyTyrIleIys 20
Db      1 ATGAGCGAAGTGGCTATTGTGTGAAAGAGGGTGGCTGCACAACAGAGGGGTACATCAAG 60

QY      21 AsnThrArgProArgTyrPheIleuIeuIystrHzAspGlySerPheIleGlyTyrIlyGln 40
Db      61 ACCTGCGGCGCACGCGTACTTCTCTCTCAAGATATAGGCACTTCATTGGCTACAAAGAG 120

QY      41 LysProGlnAspValAsp---LeuProTyrProIleuAsnAsnPheSerValAlaIysCys 59
Db      121 CGGCGCCAGAGATGTGACCAACGTAGAGCTCCCTCAACAACTTCTGTGTGGCGCAATGC 180

QY      60 GlnIleuMetIysThrGluArgProIlyAspAsnThrPheIleIleIyArgCysLeuGlnTyr 79
Db      181 CAGCTGATGAAAGCGGAGCGGCGCCGCGCAACACTTCATCATCCGCTGCTGCAAGTGG 240

QY      80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTyrThr 99
Db      241 ACCACATGTCATGGAACGCGACCTTCATGTGTGAGACTCTGTGAGCGCGGAGAGGTGACA 300

QY      100 GluAlaIleGlnAlaValAlaAspArgIleuGlnArgGlnGluGluGluIlyGlyMetAsnCys 119
Db      301 ACCGCCATCCAACTGTGTGCTGACGCGCTCAAGAAAGCAGGAGGAGAGAGATGAACTTC 360

QY      120 SerProThrSerGlnIleAspAsnIleGlyGluGluIleuMetAspAlaSerThrThrHis 139
Db      361 CGGTGGGGGTCAACCCAGTGAACAACCTCAGGGGCTGAAGAGAGAGTGTCCCTGGCCAAG 420

QY      140 HisIys---ArgIysThrMetCAsnAspPheAspTyrIleuIlybLeuLeuGlyIlyGlyThr 158
Db      421 CCCAAACACCGCGGTGACCATGAAACAGATTGATGATCACTGAAAGCTGCGGGCAAGGGCACT 480

QY      159 PheGlyIlybValIleIleuValArgGluIlyValAspGlyIlyTyrTyrAlaMetIysIle 178
Db      481 TTGGGCAAGGTATCTGTGTGAAGAGAAAGGCACAGGCGGCTATCTACGCCATGAAGATC 540

QY      179 LeuIlybGluIlyValIleIleAlaIysAspGluValAlaHisThrIleuThrGluSerArg 198
Db      541 CTCGAAGAAGAAAGTATCTGTGTGCCCAAGAGCAAGATGGCCCAACACATCAACGGAACCG 600

QY      199 ValIleuIysAsnThrArgHisProPheIleuThrSerIleuIystrYsrPheGlnThrIys 218
Db      601 GTCTCTCAAAATCTCAGAGCAACCTCTCTCAACAGCCCTGAAGTACTTTTCCAGACCCAC 660

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QY 219 AsparGLeuCySphValMetGluTyrValAsnGlyGlyGluLeuPhePheHisLeuSer 238
DB 661 GACCGCTGCTGTTTTCATGAGTACGCGCAACGGGGGAGGTGTTCTTCCACCTGTCC 720
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 721 CGGGAACGTGTGTTCTCCAGAGACCGGCGCCGCTTCTATGCGCTGAGATTGTGTACGCC 780
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 781 CTGAGCTACTGCTGACCTCGAGAAAGACGTGTGTACCGGAGCTCAAGCTGAGAAACCTC 840
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCySphGlyGlyIle 297
DB 841 ATGCTGACAGAGACCGGACATTAGATACAGACTTGGCGCTGTGCAAGAGAGGAGATC 900
QY 298 ThrAspAlaAlaThrMetLysThrPheCySphGlyThrProGluTyrLeuAlaProGluVal 317
DB 901 AAGGACGTGTCCACCATGAAAGACCTTTTGCAGCACCTGAGTACCTGCGCCCGAGAGTG 960
QY 318 LeuGluAspAspAspTyrGlyArgAlaValAspTrpGlyLeuGlyValValMetTyr 337
DB 961 CTGGAGGACAAATGACTACGCGCGTGCAGTGTGAGTGGGCGTGGCGTGGTCAATGAC 1020
QY 338 GluMetMetCySphGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
DB 1021 GAGATGATGTGGGTGCGCTGCGCTTCTTCAACACAGACCATGAGAACCTTTTATGCTC 1080
QY 358 IleLeuMetGluAspLysIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
DB 1081 ATCTCATGAGAGATCCGCTTCCGCGCACCGCTTGTCCGAGCCAAAGCTCTTGCTT 1140
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLys 397
DB 1141 TCAAGGCTGCTCAAGAAAGACCCCAAGACAGAGCTTGGGGGAGCTCCAGAGACGCAAG 1200
QY 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrArgLysLys 417
DB 1201 GAGATCATGACAGATGCTTCTTTCGCGGATGCTGTGGCAGACGCTGTACAGAAAGAG 1260
QY 418 LeuValProProPheLysProGluValThrSerGlyThrAspThrArgTyrPheAspGlu 437
DB 1261 CTCAGGCCACCTTCAAGCCCGCAGCTCAGCTCGAAGACGACACCGAGTATTTTGATGAG 1320
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1321 GAGTTCAGGCCCCAGATGATACCATCAACACCTGACCAA-----GATGACAGCATG 1374
QY 458 AspCyMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 1375 GAGTGTGTGACAGAGGAGGAGGCGCCCACTTCCCACTTCTCCACTGCGGCACG 1431

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; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Alignment Scores:
Pred. No.: 5,116-236 Length: 2184
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: Gaps: 4

US-09-869-079b-3 (1-479) x US-09-417-197-138 (1-2184)

QY 1 MetSerAspValThrIleValLysGluGlyTyrPValGlnLysArgGlyGluTyrIleLys 20
DB 742 ATGAGCGACGTGGCTATTGTGTGAAGAGGTTGGCTGCACAAACGAGGAGATGACTCAG 801
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 802 ACCTGCGCGCCACGCTACTTCTCTCTCAAGATATGACACTTCTCATTTGGCTACAGAG 861
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
DB 862 CGGCGCGAGATGTGACCAACGTGAGGCTCCCTCCCAACACTTCTCTGTGCGCAGTGC 921
QY 60 GluLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCySphGlnTrp 79
DB 922 CAGCTGATGAAACGAGAGCGGCCCGGCCCAACCTTCAATCATTCCTGCTGCAAGTGG 981
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpThr 99
DB 982 ACCACTGTCATGACGACGACCTTCCATGTGAGACTCTCTGAGAGACGAGAGAGTGCACA 1041
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCys 119
DB 1042 ACCGCGATCCACACGTGTGCTGACGCGCTCAAGAGACGAGAGAGAGAGATGACATTC 1101
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
DB 1102 CGGTGCGGCTCACCCAGTGCACACTCAGGGGCTGAAGAGATGAGAGTGTCTCTGCGCAG 1161
QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuGlyLysGlyThr 158
DB 1162 CCCAAGCACCGCGGTGACCATGAAAGATTGTGATCTCGAAGCTGCTGAGGACGACACT 1221
QY 159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIle 178
DB 1222 TTCCGCAAGGTGATCTGTGTGAAGAGAGGACAGCGCCGCTTACTTACGCCATGAAATC 1281
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
DB 1282 CTCAGAAAGAGATGATGTGTGCCAAAGACAGAGGTGGCCACACACTCACCGAAGACGC 1341
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
DB 1342 GTCCTGCAAGACTCCAGGACACCTTCTCTCAACAGCCGGAAGTACTCTTCCAGACCCAC 1401
QY 219 AsparGLeuCySphValMetGluTyrValAsnGlyGlyGluLeuPhePheHisLeuSer 238
DB 1402 GACCGCTGCTGTTTTCATGAGTACGCGCAACGGGGGAGGTGTTCTTCCACCTGTCC 1461
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 1462 CGGGAACGTGTGTTCTCCAGAGACCGGCGCCGCTTCTATGCGCTGAGATTGTGTACGCC 1521
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 1522 CTGAGCTACTGCTGACCTCGAGAAAGACGTGTGTACCGGAGCTCAAGCTGAGAAACCTC 1581
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCySphGlyGlyIle 297
DB 1582 ATGCTGACAGAGAGGAGACATTAAAGATCAACAGCTTCCGCGCTGTGCAAGAGAGGAGATC 1641

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Qy 298 ThrAspAlaIaThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluVal 317
Db 1642 AAGGACGGTGCACCAAGAAAGACCTTTGGGCGACACCTGAGTACCTGGCCCCGAGAGT 1701
Qy 318 LeuGluAspAsnAspTrpGlyArgAlaValAspTrpGlyLeuGlyValAlaMetTyr 337
Db 1702 CTGAGGACCAATGACTACGGCCGTCGAGTGGACTGGTGGGGCTGGGGCTGGTCACTTAC 1761
Qy 338 GluMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
Db 1762 GAGATGATGTGGCGTCCCTGCTTCTTACAAACAGACCATGAGAGCTTTTGGAGCTC 1821
Qy 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1822 ATCTCATGGAGAGATCCCTTCCCGGACGCTTGCTCCGAGGCAAGTCTTGCTT 1881
Qy 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
Db 1882 TCAGGCGTCTCAAGAAAGACCCCAAGACAGCTTGCGGGGCTCCGAGAGCCAG 1941
Qy 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLys 417
Db 1942 GAGATCATGACGATCCCTTCTTGCGGATCGTGGCAGCAGTGTACGAGAGAGAG 2001
Qy 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437
Db 2002 CTAGCCGACCTTCAAGGCCCCAGGTACGTGGAGCTGACACAGATTTTGTAGTAG 2061
Qy 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
Db 2062 GAGTTCAGCGGCCAGATGATCACCATCACACCACTACCA-----GATGACAGCATG 2115
Qy 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
Db 2116 GAGGTGTGGACAGCAGGAGCGGACCCACTTCCCGAGTTCTCTACGCGCAGC 2172

RESULT 5

US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212, 771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Alignment Scores:

Pred. No.:	6,736-236	Length:	2610
Score:	2099.50	Matches:	396
Percent Similarity:	90.19%	Conservative:	36
Best Local Similarity:	82.67%	Mismatches:	42
Query Match:	82.08%	Indels:	5
DB:	2	Gaps:	4

US-09-869-079b-3 (1-479) x US-09-212-771-1 (1-2610)

Qy 1 MetSerAspValThrIleValLysGluGlyTyrValGlnLysArgGlyLysTyrIleLys 20
Db 199 ATGGGCAACGTGGCTATTGTGAAGAGAGGTTGGCTGCACAAACGAGGGAGTACATCAAG 258
Qy 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspLysSerPheIleGlyTyrLysGlu 40

Db 259 ACCTGGCGGCGACGCTACTTCTCTCAAGAAAGTGGACCTTACTGGCTCAAGAG 318
Qy 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
Db 319 CGGCCCCAGGATGTGACCAACGTGAGGCTCCCTCAACAACACTTCTGTGGCGGAGTGC 378
Qy 60 GluLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79
Db 379 CAGCTATGAAAGCGAGCGGCCCCCGCCCAACCTTCACTACCTGCTGCTGCAAGTGG 438
Qy 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpTrp 99
Db 439 ACCACTGTCAATGAAAGCGACCTTCCATGTGGAATCTCTGAGAGCGGAGAGGTGACA 498
Qy 499 ACCGCGATCCAGACTGTGGCTGACGCGCTCAAGAACAGAGAGAGAGATGACTTC 558
Db 120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrHis 139
Qy 559 CGGTGGGCTCACCCAGTACAACTCAGGGGCTGAAGAGATGGAGTGTCTGCGCAAG 618
Db 140 HisLys---ArgLysThrMetAspAspPheAspTyrLeuLysLeuGlyLysGlyThr 158
Qy 619 CCAGAGCAGCGGTGACCAATGAAAGAGTTGAGTACTTGAAGCTGTGGAGAGGAGCT 678
Qy 159 PheGlyLysValIleLeuValArgLysLysAspGlyLysTyrTyrAlaMetLysIle 178
Db 679 TTGGGAGAGGTATCTGTGGTGAAGAGAGGACAGGCGCGTACTACGCGATGAAGATC 728
Qy 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
Db 739 CTCMAAGAGAAATCATCTGTGGCAAGAGAGAGAGTGGCCACATCCACCGAAGCCGG 798
Qy 199 ValLeuLysAsnThrArgHisAspProPheLeuThrSerLeuLysTyrSerPheGlnTrpLys 218
Db 799 GTCTCGAGAACTCCAGGACCCCTTCTCACAGCCCTGAAGTACTTTCCAGACCAC 858
Qy 219 AspArgLeuCysAspPheValMetGluTyrValAsnGlyGlyLeuPhePheHisLeuSer 238
Db 859 GACCGCTCTGCTTGTTCATGAGGTACGCCAACAGGGGGAGAGTGTCTTCCACTGTC 918
Qy 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
Db 919 CGGGAACGTGTCTCCAGAGACCGCGCCGCTTGTATGGCGCTAGATGTGTAGCC 978
Qy 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
Db 979 CTGGACTTACTGACTCGGAGAAAGACGTGGTGTACCGGACCTCAAGCTGAGAACTTC 1038
Qy 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
Db 1039 ATGCTGGAACAAGAGCGGACATTTAGATCACAGACTTGGGGTGTGCAAGAGGGAGATC 1098
Qy 298 ThrAspAlaIaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
Db 1099 AAGGACGTTGCCCACTGAAGACCTTTTGGCGACACTGAGTACTGCGCCCCGAGAGTG 1158
Qy 318 LeuGluAspAsnAspTrpGlyArgAlaValAspTrpGlyLeuGlyValAlaMetTyr 337
Db 1159 CTGGAGGACAAATGACTACGCGCGTGAAGTGAAGTGGGGGCTGGGCTGATGTAC 1218
Qy 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
Db 1219 GAGATGATGTGGGTGCTGCTGCTTCTCAACAGAGACATGAGAGAGCTTTTGTAGCTC 1278
Qy 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1279 ATCTCATGAGAGAGATCCGCTTCCGCGACGCTTGTGTCGAGGCGCAAGTCTTGCTT 1338
Qy 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397

Db 1339 TCAGGCTGCTCAAGAGCAAGCCCAAGCAGAGCTTGGCGGGGCTCCGAGAGCCCAAG 1398
QY 398 GUAUleMeArghIsesrPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLys 417
Db 1399 GAATCATGACGATCGCTTCTTTCGGGTATCTGTGGCAGCATGTAACGAAGAAG 1458
QY 418 LeuValProProPhePheProGlnValThrSerGlnThrAspThrArgTyrPheAspGlu 437
Db 1459 CTCAGCCCACTTCAAGCCCAAGCTGACGTCCGAGACTGACACCAAGTATTTGATGAG 1518
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGlnLysTyrAspGluAspGlyMet 457
Db 1519 GAATTACCGCCCAAGATGATGATCACCATCAACCACTGACCA-----GATGACAGCATG 1572
QY 458 AspCyMeArAspAsnGlnArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
Db 1573 GAGTGTGTGACAGCAGGAGCCAGGCCCTTCCCAAGTTCTCTCACTGCGCCAGC 1629
RESULT 6
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091, 058
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ. ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1
Alignment Scores:
Pred. No.: 6 73e-236 length: 2610
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 3 Gaps: 4
US-09-869-079b-3 (1-479) x US-09-091-058-1 (1-2610)
QY 1 MeSerAspValThrIleValLysGlnGlyTyrValGlnLysArgGlyGlyTyrIleLys 20
Db 199 ATGAGCGACGTGCTATTTGGAAGAGGTTGGCTGACAAACGAGGAGATCATCAAG 258
QY 21 AsnTrpArgProArgTyrPheLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
Db 259 ACCTGGCGGCGCAAGTCTCTCCCAAGATGATGACCTTCATTTGGCTTCAAGAGAG 318
QY 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
Db 319 CGGCCGACGATGTGACCAACGTGAGCTCCCTCAACACTTCTCTGTGGCGCAGTGC 378
QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79
Db 379 CAGCTGATGAAGACGAGCGCGCCCGCCCAACACCTTCATTCGCTGCGTGCAGTGG 438
QY 80 ThrThrValIleGlnArgThrPheHisValAspThrProGlnGlnArgGlnGlnTrpThr 99
Db 439 ACCACTGTATCGAAGCAGCACTTCCATGTGAGACTTCCTGAGAGCGGGGAGTGGACA 498

QY 100 GUAUAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlnGlnLysArgMetAsnCys 119
Db 499 ACCGCCATTCAGACCTGTGGCTTACCGGCTCAAGAAAGCAGAGAGAGATGACTTC 558
QY 120 SerProThrSerGlnIleAspAsnIleGlyGlnGlnGlnGlnGlnGlnGlnGlnGln 139
Db 559 CGGTGGGCTCAACCAAGTACCACTCAGGGGCTGAAGATGAGATGAGTGTCTTGGCCAA 618
QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLysLysLeuLysGlyArgGlyThr 158
Db 619 CCAAGACACCGGTGACCAAGACAGATTTGATGATCTGAACTCTGAGCAAGGACT 678
QY 159 PheGlyLysValIleLeuValArgGlnLysAlaSerGlyLysTyrTyrAlaMetLysIle 178
Db 679 TTCGCAAGATGATCTGTGTAAGAGAAAGCCACAGCCGCTTACCGCATGAAGATC 738
QY 179 LeuLysLysGlnValIleIleAlaLysAspGlnValAlaHisPheThrGlnSerArg 198
Db 739 CTCAGAAAGAGATCATCGTGGCCAAAGCAGAGTGGCCACACACTCACAGAAACCGC 798
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
Db 799 GTCTGCAAGACTCAAGCAGCCCTTCTCACAGCCCTGAAGTACTTTCACAGACCCAC 858
QY 219 AspArgLeuCyPhePheValMetGlnTyrValAsnGlyGlyGlnLysPheHisLeuSer 238
Db 859 GACCCGCTGTGTTGTGATGAGATACGCCAACGGGGGGAGCTGTCTTCACCTGTCC 918
QY 239 ArgGlnArgValPheSerGlnAspArgThrArgPheTyrGlyAlaGlnIleValSerAla 258
Db 919 CCGGAACGTGTGTTCTCCAGAGACCGGGCCCTTCTATGCGCTGAGATTTGTCCAGCC 978
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGlnAsnLeu 277
Db 979 CTGACTACTCTCACTCGAGAAAGACGGTGTACCGGAGCTCAAGCTGAGAACTTC 1038
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlnLysIle 297
Db 1039 ATGCTGACAAAGAGAGCGGACATTAAGATCAACAGCTTGGCTGTGACAGAGGGATC 1098
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGlnTyrLeuAlaProGlnVal 317
Db 1099 AAGGACGGTGCACATGATGACCTTTGGCCGACACCTGATCTGGCCCCCAGAGTG 1158
QY 318 LeuGlnAspAspAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlnValValMetTyr 337
Db 1159 CTGAGAGCAATGACTACGCGCTGACAGTGTGAGTGTGAGTGTGATCATGTAC 1218
QY 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGlnLeu 357
Db 1219 GAGATGATGTGGGTGCTGCTGCTTCTTACCAACAGACAGACGATTTTGAAGTCC 1278
QY 358 IleLeuMetGlnAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1279 ATCTCATGAGAAATGATCTGCTCCGCGCAAGCTTGGTCCGAGGCCAAGCTTGTGCTT 1338
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
Db 1339 TCAGGCTGCTCAAGAGAGCCCAAGCAGAGCTTGGGGGGGCTCCGAGAGCGCAAG 1398
QY 398 GUAUleMeArghIsesrPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLys 417
Db 1399 GAATCATGACGATCGCTTCTTTCGGGTATCTGTGGCAGCATGTAACGAAGAAG 1458
QY 418 LeuValProProPhePheProGlnValThrSerGlnThrAspThrArgTyrPheAspGlu 437
Db 1459 CTCAGCCCACTTCAAGCCCAAGCTGACGTCCGAGACTGACACCAAGTATTTGATGAG 1518
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGlnLysTyrAspGluAspGlyMet 457
Db 1519 GAGTGTGTGACAGCAGGAGCCAGGCCCTTCCCAAGTTCTCTCACTGCGCCAGC 1572


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Qy      458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
Db      1573 GAGGTGTGGACGACGACGCGACCCACCTTCCCCAGTTCTCTACTCGGCGACG 1629

RESULT 7
US-09-023-655-1206
/ Sequence 1206, Application US/09023655
/ Patent No. 6607879
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/ APPLICANT: Susan G. Stuart
/ APPLICANT: Jeffrey J. Seilhamer
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
/ NUMBER OF INVENTION: EXPRESSION
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/023,655
/ FILING DATE: HEREMITH
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ REFERENCE/DOCKET NUMBER: PA-0001 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 1206:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2610 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: g190827
/ US-09-023-655-1206

Alignment Scores:
Pred. No.: 6,73e-236 Length: 2610
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 4 Gaps: 4

US-09-869-079b-3 (1-479) x US-09-023-655-1206 (1-2610)

Qy      1 MetSerAspValThrIleValIleGluGlyTyrValGlnIleValArgGlyIleValIleVal 20
Db      199 ATGAGCAGCGTGGCTATTGTGAAGAGGAGGTGGCTGCACAAACGAGGAGATCATCAG 258

Qy      21 AsnTyrArgProAspGlyTyrPheLeuLeuIleThrAspGlySerPheIleGlyTyrIleValGlu 40
Db      259 ACCGTGGGCGCACGCTACTCTCTCTCAAGAAATATGACACCTTCATTTGGCTACAGAGAG 318

Qy      41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaIleValCys 59
Db      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db      319 CGGCGCGAGGATGNGACCAAGCNGAGGCTCCCTCAACAACCTTCTGTGGCGACATGC 378
Qy      60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleLeuValIleValIleVal 79
Db      379 CAGCTGATGAAGACGAGCGGCGCCCGCCCAACCTTCATCTCCGCTCCGTCGACATGG 438

Qy      80 ThrValIleIleGluArgThrPheHisValAspThrProGlnGluArgGluIleValIleVal 99
Db      439 ACCACTGTCAATCAAGACGACCTTCCATGTGAAGCTCTGAGAGCGGAGGAGATGACCA 498

Qy      100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluIleValIleValIleVal 119
Db      499 ACCGCATTCAGACTGTGGCTGACGGCTCTCAAGAGAGAGAGAGAGAGATGACATTC 558

Qy      120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetLeuAlaSerThrThrHis 139
Db      559 CGGTGGGCTCACCGACGTGCAACTCAGGGGCTGAAGATGAGGTGCTCCGCGCCAG 618

Qy      140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluIleValIleVal 158
Db      619 CCAGAGCAGCGCTGACCATGAAGAGTTTGAGTACCTGAAGCTGTGGAGAGGAGCT 678

Qy      159 PheGlyLysValIleLeuValArgGluLysValAspSerGlyLysTyrTyrAlaMetLysIle 178
Db      679 TTCGGCAGAGTATCTCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATC 738

Qy      179 LeuLysLysGluValIleIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
Db      739 CTCAGAGAGAGAGATCATCTGTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798

Qy      199 ValLeuLysAsnThrArgHisPhePheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
Db      799 GTCTGAGAGACTCCAGAGACCCCTTCTCTCAGAGCTGAGTACTTTCACAGACCAC 858

Qy      219 AspArgLeuCysPheValMetGluTyrValAsnGlyGlyLeuPhePheHisLeuSer 238
Db      859 GACCGCTCTGCTTTCATGAGATGAGCAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 918

Qy      239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyValGluIleValIleVal 258
Db      919 CGGGAAGTGTGTCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978

Qy      259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuValIleVal 277
Db      979 CTGACTACCTGACTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038

Qy      278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluIleVal 297
Db      1039 ATCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098

Qy      298 ThrAspAlaIleThrMetLysThrPheCysGlyTyrProGluTyrLeuAlaProGluVal 317
Db      1099 AAGAGCGTGCACCATGAAGACCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158

Qy      318 IleuGluAspAsnAspArgTyrArgAlaValAspTyrTyrGlyLeuIleValIleValMetTyr 337
Db      1159 CTGAGAGACAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218

Qy      338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
Db      1219 GAGATGATGTGGCGTGGCTGCTCTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278

Qy      358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db      1279 ATCTCATGAGAGAGATCGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1338

Qy      378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyIleValProAspAspAlaLys 397
Db      1339 TCAGGCTGTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398

Qy      398 GluIleMetArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLys 417
Db      1399 GAGATCATGAGATGCTTCTTTCGCGGATTCGTGTGACAGAGAGAGAGAGAGAGAGAG 1458

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; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
; US-09-256-465-1

Alignment Scores:
Pred. No.: 5,156-225 Length: 1599
Score: 2004.00 Matches: 374
Percent Similarity: 88.84% Conservative: 56
Best Local Similarity: 77.27% Mismatches: 46
Query Match: 78.34% Indels: 8
DB: 3 Gaps: 5

US-09-869-079b-3 (1-479) x US-09-256-465-1 (1-1599)

QY 1 MetSerArgValThrIleValIysGluGlyTrpValGlnIysArgGlyIuTyrlleLys 20
DB 88 ATGATAGAGTGTCTGTCATCAAGAGAGGCTGCTCCACAGAGCGTGGTAATACATAG 147
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspLysSerPheIleGlyTyrLysGlu 40
DB 148 ACGTGAGGCGCAGCGTACTCTCGCTGAGAGCGAGCGCTCTTCATTTGGGTACAGAG 207
QY 41 LysProGln-----AspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLys 58
DB 208 AGCGCCGAGGCGCCCTGATCAGACTCTACCC---CCCTTAACAACCTTCCTGTAAGCAGAA 264
QY 59 CysGlnIleuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysIleuGln 78
DB 265 TGGCAGCTATGAGAGCCGAGAGCGCGGACCCACACCTTTGTCATACCTGCTGCAG 324
QY 79 TrpThrValIleGluArgThrPheIleValAspThrProGluGluArgGluGluTrp 98
DB 325 TGGACCACTGATCGAGAGAGACCTTCACGTGATTCTCCAGACGAGAGGAGAGTG 384
QY 99 ThrGluAlaIleGlnAlaValAlaAspArgLysGlnArgGlnGlu-----GluGluArg 116
DB 385 ATCGGCGCCATCCAGATGATGCGCCACAGCCCTCAAGAGCGGCGCCACGAGGAGACCC 444
QY 117 MetAsnCysSerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSer 136
DB 445 ATGGAATCAAGTGTGCTCCCGCAGTACTCTCCACGACTGAGGAGATGAGAGTGCG 504
QY 137 ThrThrIshIleuArgLys---ThiMetAsnAspPheAspTyrIleuLysIleuGly 155
DB 505 GTGAGCAAGGCGAGCGGTAAAGTACCATGATGACTTCACATCTCAATCTCTTGGC 564
QY 156 LysGlyThrPheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAla 175
DB 565 AAGGGAACCTTTGGCAAGTCACTCTGCTCGGAGAGGCACTGCGCCCTACTAGCC 624
QY 176 MetLysIleuLysLysGluValIleIleAlaLysAspGluValAlaIshIleuThr 195
DB 625 ATGAAATCTCTGCAAGAGAGTCAATATGCGCAAGATGAGTCAACAGTCAACAGTACC 664
QY 196 GluSerArgValIleuLysAsnThrArgIshProPheLeuThrSerLeuLysTyrSerPhe 215
DB 685 GAGAGCGCGGTCTCTCCAGAACACAGGCAACCGTCTCTCACTGCGGAGATGCTTCC 744
QY 216 GlnThrLysAspArgLysCysPheValMetGluTyrValIshGlyGluLeuPhe 235
DB 745 CAGACCCACACAGCGCTGTGCTTGTGATGAGATGCCAACGCGGCTGAGCTGCTTCC 804
QY 236 HisLeuSerArgLysArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIle 255
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DB 805 CACCTGCCCCGAGGCTGCTTACAGAGAGCGGCGCGTTTATGTCAGAGATT 864
QY 256 ValSerAlaLeuAspTyrIleuHisSerGlyLysIleValTyrArgAspLeuLysGlu 275
DB 865 GTCTCGGCTCTTGAAGTACTGCACTCGCGGAGCGTGTATACCGGACATCAAGCTGAA 924
QY 276 AsnLeuMetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlu 295
DB 925 AACCTATGCTGAGCAAGATGGCCACATCAATATCACTGACTTGGCTTCGCAAGAG 984
QY 296 GlyIleThrAspAlaIshThrMetLysThrPheCysGlyThrProGluTyrIleuAlaPro 315
DB 985 GGCATCAGTACGAGGCGCCACATGAAACCTTCTGTGGACCCCGAGTACTGCGGCGCT 1044
QY 316 GluValIleuGluAspAsnAspTyrGlyArgAlaValAspTrpTrpLysGlyValI 335
DB 1045 GAGGTCTGAGAGCAATGACTATGCGCGGCGCTGGAAGTGTGGGGCTGGTGTGTC 1104
QY 336 MetTyrGluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPhe 355
DB 1105 ATGTACGAGATGATGTGCGCGCGCTGCGCTCTTACACAGGACACAGAGCGCTTTC 1164
QY 356 GluLeuIleuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSer 375
DB 1165 GAGCTATCTCTATGAGAGAGATCCGCTTCCGCGAGCGTCCAGCCCGAGGCGCAAGTCC 1224
QY 376 LeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAsp 395
DB 1225 CTGCTTGCGGCTGTCTTAAGAGAGACCCAGCAGAGGCTGTGTGGGGGCCACAGAT 1284
QY 396 AlaLysGluIleuMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAsp 415
DB 1285 GCCAAGAGGTCTATGAGACAGAGTCTTCTCAGCATCAATCGGAGAGACGTTGTCAG 1344
QY 416 LysLysLeuValProProPheLysProGlnValIshThrSerGlyThrAspThrArgTyrPhe 435
DB 1345 AAGAACTCTCTGCAACCTTCAACCTCAAGTCACTCGAGGTGACACAGAGTACTTC 1404
QY 436 AspGluGluPheThrAlaGlnThrIleThrIleThrProGluLysTyrAspGluAsp 455
DB 1405 GATGAGTAATTTACCGCCCATCATCATCAATCAACACCCCTGACCGCTATGACAGCTG 1464
QY 456 GlyMetAspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAla 475
DB 1465 GGCCTTA-----CTGAGGCTGACACGAGCGAGCCAGCTCCCGCATTTCTACTCGGCC 1518
QY 476 SerGlyArgGlu 479
DB 1519 AGCATCCGCGAG 1530

RESULT 10
US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavoigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/167,322
3 FILING DATE: 07-Oct-1998
4 CLASSIFICATION: <Unknown>
5
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: PCT/US97/00582
8 FILING DATE: <Unknown>
9
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Monaco, Daniel A.
12 REGISTRATION NUMBER: 30,480
13 REFERENCE/DOCKET NUMBER: 7933-33 PC
14
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (215) 568-8383
17 TELEFAX: (215) 568-5549
18
19 INFORMATION FOR SEQ ID NO: 3:
20
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 1599 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26
27 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
28
29 US-09-167-322-3

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Alignment Scores:	
Pred. No.:	5,15e-225
Score:	2004.00
Percent Similarity:	88.84%
Best Local Similarity:	77.27%
Query Match:	76.34%
DB:	3
US-09-869-0798-3 (1-479) x US-09-167-322-3 (1-1599)	
	Length: 1599
	Matches: 374
	Conservative: 56
	Mismatches: 46
	Indels: 8
	Gaps: 5

US-09-869-079B-3 (1-479) x US-09-167-322-3 (1-1599)

QY	MeSerAspValThrIleValIysGluGlyTPVAlGlnLysArgGlyGluTyrIleLys	20
Db	ATGAATAGAGGTGTCTGTCAATCAAGAGAGCTGGCTCCACACCGTGGTAATACATCAAG	14
QY	AsnTPArpProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu	40
Db	ACCTGGAGGCGCACGGTACCTTCCTGGTAAGAGAGAGCGGCTCTTCAATTGGGTACAAGAG	20
QY	LysProGln-----AspValAspLeuProTyrProLeuAsnAspSerValAlaLys	58
Db	AGGCCCCGAGGCCCCCTATCAGACTACACCC-----CCCTTAAACACTTCCGTACAGAA	26
QY	CysGluLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGln	78
Db	TGCCAGCTGATGAAGACCGAAGAGCGGACCCACACTTGTATACGCTGGCTGGAG	32
QY	TyrThrThrValIleGluArgTyrThrPheIleValAspThrProGluGluArgGluTyr	98
Db	TGGACCACTGATTCGAGAGGACTTCCACGTGGATTCCTCCAGAGAGAGAGGAGAGTGG	38
QY	ThrGluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlu-----GluGluArg	116
Db	ATGGGGGCGCATCCAGATGTGCGCCAACACTTCAGCAGCGGGCCCCAGCGAGAGCCCC	44
QY	MetAsnCysSerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSer	134
Db	ATGACATCAACAAGTGTGGCTCCGCCAGTACTCTCCACGACTGAAGAGATGGAAGTGGCG	50
QY	ThrThrHisIleIleAspArgLys--ThrMetAsnAspPheAspTyrLeuLysLeuGly	152
Db	GTCAGCAAGGCACAGGGCTAAAGTGAACATGAATGACTTGACTTCAACTCCTTGGC	56
QY	LysGlyThrPheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAla	170
Db	AAGGGAACCTTTGGCAAGATCATCTCGTGGCGGAGAGGCCACTGCGCGCTACTAGCCG	62
QY	MetLysIleLeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThr	190
Db	ATGAAGTCTCTGGAAAGGAAGTCAATTCATTCGCAAGAGTGAAGTGTGCTCAACAGTACC	68

OY		196	G l u s e r t y g v a l l e u s p a n t h r a x h i p r o p h e u t h s e r l e u s y r s e p h e	215
OY		197	216
D b		685	G A G A C C G G G G T C C C A G A A C A C C A G G A C C C G T T C T A C T G C G C G A A G T A T G C C T T C	744
OY		216	G l n t h r l y s a p a r g l e u c y s p h e v a l m e t g l u t y r v a l a n g l y g l j u l e u p h e	235
D b		745	C A G A C C A C A G A C G C C T G T G C T T G T A T G A G A T A T C C A A C G G G G G T G A G C T T G T T C C	804
OY		236	H i s l e u s e r t a r g l u a t a g v a l p h e s e r g l u a s p a r g h r z a r p h e t y r g l y a l a g l i l e	255
D b		805	C A C C T G T C C G G G A G C G T G C T T C A C A G A G A G A G G G G C C G G T T T A T T G G T G A G A G A T T	864
OY		256	V a l s e r a l a l e u a p p y r l e u h i s s e r g l y l e s t l e v a l t y r a r g a p s e l e u s y l e u g l u	275
D b		865	G T C T C G G C T T T A G T A C T T G C A C T C G C G G A G C G T G A T A A C C G A C A T C M A G C T G A A	924
OY		276	A s n l e u m e t l e u a p p l y a a p g l y h i s l e l y s l l e t h r a p h e c i j l e u c y l y s g l u	295
D b		925	A A C C T A T G C T G A C A A A G A T G G C A C A T C A A G A T C A C T A C T T T G G C C T T G C G A A A G A G	984
OY		296	G l y l l e t h r a p a l a a l a t r m e t l y s t h r p h e c y s g l y t h r p r o g l u t y r l e u a l a p r o	315
D b		985	G G C A T C A G T A C G G G G C A C C A T A G A A A C C T T C T G T G G A C C C C G G A G T A C T T G C G C C C T	1044
OY		316	G l u v a l l e u g l u a s p a n a p p y r g l y a r g l a v a l a s p t r p r t p r g l y l e u g l y v a l v a l	335
D b		1045	G A G T G C T C G A G A C A A T A G C T A T G C C G G G C C G T G A C T G T G G G G G C T G G G T G T G T C	1104
OY		336	M e t t y r g l u m e t m e t c y s g l y a r g l e u p r o p h e t y r a n g l n a p h i s g l u l y b l e u p h e	355
D b		1105	A T G T A C G A G A T A G A T G T G G G C C G C C T G C C C T T C A C A A C C A G A C C A C G A G C G C T T T C	1164
OY		356	G l u l e u l l e u m e t g l u a p p l l e l y s p h e p r o a r g t h r l e u s e r s e r a p a l a l y s e r	375
D b		1165	G A G C T C A T C C C A T G A G A A G A G A T C C G C T T C C C G G C A C G C T C A G C C C G A G G C C A A G T C C	1224
OY		376	L e u l e u s e r g l y l e u l e u l l e l y a s p p r o a n l y s a r g l e u g l y g l y g l p r o a p a s p	395
D b		1225	C T G C T T C T G G G C T G C T T A A G A A G A G A C C C A G A G A G S C T T G T G G G G G A C C C A G C A T	1284
OY		396	A l a l y s g l u l l e m e t a r g h i s s e r p h e s e r g l y a l a n t p o j n a p v a l t y r a s p	415
D b		1285	G C C A A G A G A G G C A T G A G A C A C A G T T T C T C A G C A T C A A C T A G C A G A C G T G T C A G	1344
OY		416	L y s l y s l e u v a l p r o p r o p h e l y s p r o g l n v a l t h s e r g l u t h r a s p t h r a r g t y r p h e	435
D b		1345	A A G A A G C T C C G C A C C C T T C A A A C C T C A G T C A C G T C C A G A G C G A C A C A A G A G T A C T T C	1404
OY		436	A s p o l u g l u p h e m t r a l a g l n t h r l l e t h r l l e t h r p r o p r o g l u s t y r a a p g l u a s p	455
D b		1405	G A T A T A A A T T A T T A C C G C C A G T C A T C A T C A C A C C C C T T A G C C C T A T G A C A G C C T G	1464
OY		456	G l y m e t a p c y m e t a p a n g l u a r g a r p r o h i s p h e p r o g l n p h e s e r t y r s e r a l a	475
D b		1465	G G C T T A ----- C T G A G A C T G A C A C C A G A C C A C C A C T T C C C A G T T C T C T A C T G G C C	1518
OY		476	S e r g l y a r g l u	479
D b		1519	A G C A T C C G C G A G	1530
RESULT 11				
/ US-09-023-1004				
/ Sequence 1004, Application US/09023655				
/ Patent No. 6607879				
/ GENERAL INFORMATION:				
/ APPLICANT: Coeks, Benjamin G.				
/ APPLICANT: Susan G. Stuart				
/ APPLICANT: Jeffrey J. Sellhammer				
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE				
/ NUMBER OF INVENTION: EXPRESSION				
/ NUMBER OF SEQUENCES: 1508				
/ CORRESPONDENCE ADDRESS:				
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.				


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RESULT 12
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3

Alignment Scores:
Pred. No.: 4,72e-201 Length: 1254
Score: 1798.50 Matches: 342
Percent Similarity: 89.45% Conservative: 31
Best Local Similarity: 82.01% Mismatches: 39
Query Match: 70.31% Indels: 5
DB: 4 Gaps: 4

US-09-869-079B-3 (1-479) x US-09-590-740-3 (1-1254)

QY 62 MetLysThrGluArgProLysProAsnThrPheIleArgCysLeuGlnTrpThr 81
DB 1 ATGAAGACGAGGAGGCGCGCCCAACACCTTCATCATCGCGCTCGAGTGAGCACT 60
QY 82 ValIleGluArgThrPheHisValAspThrProGluGluArgGluGlnTrpThrGluAla 101
DB 61 GTCATCGAAGCACTTCATCATGTGAGACTCTCTGAGAGCGGAGAGAGTGAACAACCGCC 120
QY 102 IleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSerPro 121
DB 121 ATCCAGACTGTGGCCGACCGCTCAAGAAAGCAGAGAGAGAGATGAGACTTCCGGTGC 180
QY 122 ThrSerGlnIleAspAsnIleGluGluGluMetAspAlaSerThrTrHisIleLys 141
DB 181 GGCTACCCAGCGACAACTCAGGGGCGCAAGATGAGAGTGCCTGGCCAAAGCCCAAG 240
QY 142 ---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGluLysGlyThrPheGly 160
DB 241 CACCGCGTGACCATGAACGATTTGATGCTGAACTGCTGGGCAAGGCGACTTTCGCG 300
QY 161 LysValIleLeuValArgLysValAspSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 301 AAGGTATCTCTGTGAAGAGAGAGCCACAGCG--TACTAGCCCATGAAATCTCTCAG 357
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 358 AAGGAAGTATGTCGTGGCCAAAGACGAGTGGCCCAACACTACCGAAGAACCGGTCAG 417
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 418 CAGAACTCCAGGACCCCTCTCTCACTCCCTGAATACTCTTTCAGACCCACGACCGC 477
QY 221 LeuCysPheValMetGluTyrValAlaAsnGlyGlyLeuPhePheHisLeuSerArgGlu 240
DB 478 CTCCTGCTTTGTATGAGTACGCAACGAGGAGGAGCTGTTCTTCCACTGTCGCGGAG 537
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB 538 CGATGATTCGCGAGAGACCGGCGCGCTTCTATGCGCTGAGATTGTGTACAGCCCTGAG 597
QY 261 TyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeuMetLeu 279
DB 598 TACCTGCACTCGAAGAAAGACGTGTATCGGGACCTCAAGCTGAGAACTCATGTCTG 657
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QY 280 AspLysAspGlyHisIleIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAsp 299
DB 658 GACAAAGACGCGGACATTAAGATCAACACTTCGCGGCTGTGCAAGAGGAGATCAAGAC 717
QY 300 AlaAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGlu 319
DB 718 GGTGCACCATTAAGACCTTTTGGCGGACACCTGAGTACTTGGCCCGGAGGTGTGAGG 777
QY 320 AspAsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGluValValMetTyrGluMet 339
DB 778 GACAAATGACTAGCGCGGTGACAGTGAAGTGGGAGGCTGGGCGGTGATGATGACAGAGT 837
QY 340 MetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuLeu 359
DB 838 ATGTGCGGTGCGCTCCCTCTTCAACAACAGACCATGAGAGCTTTTGAAGCTCATCTTC 897
QY 360 MetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGly 379
DB 898 ATGAGAGAGATCCGCTCCCGGACGCTTGATCCCGAGGCCAAGTCTTGCTTCAAGG 957
QY 380 LeuLeuIleLysAspProAsnLysArgLeuGlyGlyTyrProAspAspAlaLysGluLeu 399
DB 958 CTGCTCAAGAAAGACCCCAAGCAGAGGCTTGCGGAGGCTCGAGCAGCGCCAAAGAGATC 1017
QY 400 MetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLeuVal 419
DB 1018 ATGCAAGATCGCTTTTACCGGTATCGTGGCGACGACGCTTACGAGAAGAGCTCAGC 1077
QY 420 ProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGluGluPhe 439
DB 1078 CCACCTTCAAGCCCAAGGTCACTGCGAGACTGACACAGGATATTTGATGAGAGTTC 1137
QY 440 ThrAlaGlnThrIleThrIleThrProGluLysTyrAspGluAspGlyMetAspCys 459
DB 1138 ACGGCCAGATGATCAATCAACACTGACCA-----GATGACAGCATGAGATGT 1191
QY 460 MetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 1192 GTGACAGAGAGCGAGGCGCCCACTTCCCGCAAGTCTCTACTCCGCCAGC 1242

RESULT 13
US-10-067-977-1
; Sequence 1, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-977-1

Alignment Scores:
Pred. No.: 2.1e-97 Length: 1338
Score: 916.00 Matches: 193
Percent Similarity: 60.75% Conservative: 67
Best Local Similarity: 45.09% Mismatches: 140
Query Match: 35.81% Indels: 28
DB: 4 Gaps: 7

US-09-869-079B-3 (1-479) x US-10-067-977-1 (1-1338)

QY 53 AsnPheSerValAlaLysCysGlnLeuMetLysThrGluArgProLysProAsnThrPhe 72
DB 53 AsnPheSerValAlaLysCysGlnLeuMetLysThrGluArgProLysProAsnThrPhe 72
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Db 97 TCCTTCCTGCTGACGGAGCTGGCTTTCATGAGACAGAGAGATGGGTCTGACGACTT 156
 QY 73 ILeIeArgCysLeuGlnTrpThrValIleGluArgThrPheHisValAspThrPro 92
 Db 157 ATTACAGAAAG-----ATTGCCAATTAATCTCATGATGATCAAAACACCTT 198
 QY 93 GluGluArgGluGluTrpThrGluAlaIleGlnAlaValAlaAspArgLeuGlnArgGln 112
 Db 199 GAA-----GTTCAAGTCATCTTGAAAGATCTCCCAACCTGAG 234
 QY 113 GluGluGluArgMetAspCysSerProThr-----SerGlnIleAspAsn 127
 Db 235 GAGCCTGAGCTTATGATGATGACCACTTCTCTCCACCAAGCTCTTTCAGCAATAC 294
 QY 128 ILeGlyGluGluGluMetAspAlaSerThrThrHisIleValArgGlySerMetAspAsp 147
 Db 295 CTGGC-----CCGTGCTCAATCTCATGCTCTAA-----CCATCTGAC 333
 QY 148 PheAspTrpLeuLeuLeuLeuGlyValGlyThrPheGlyValIleLeuValArgGlu 167
 Db 334 TTTCACCTTCTTGAAAGATGATCGAAGAGGAGATTGGAAAGTTCTTTCAGCAAGAC 393
 QY 168 LysAlaSerGlySerTrpTrpAlaMetValIleLeuValArgGluIleIleAlaLys 187
 Db 394 AAGGCAGAAAGAGTCTTATGCACTCAATGTTTACAGAAAGAAAGCAATCTCGAAAG 453
 QY 188 AspGluValAlaHisThrLeuThrGluSerArgVal---LeuLysAsnThrArgHisPro 206
 Db 454 AAAGAGAGAGACATATTATGTCGACCGAATGTTCTGTTGAAGATGGAAGACACCT 513
 QY 207 PheLeuThrSerLeuSerTrpSerPheGlnThrLysAspArgLeuCysPheValMetGlu 226
 Db 514 TTCTCTGGTGGCCCTTCACTTCTTCTTCAACCTGCGAATTTGACTTGTTCCTAGAC 573
 QY 227 TyrValAsnGlyGlyGluLeuPhePheHisLeuSerArgGluArgValPheSerGluAsp 246
 Db 574 TACATTAATGATGAGAGTGTCTTCTTACATCTCCAGAGGAAACCTGCTTCTCGGAACA 633
 QY 247 ArgThrArgPheTrpGlyAlaGluIleValSerAlaLeuAspTrpLeuHisSerGlyLys 266
 Db 634 CGGGCTCGTTTCTATGCTGCTGAAATGCGAGTCCCTGGGCTACGCAATTCACCTGAC 693
 QY 267 ILeValIleValIleValIleValIleValIleValIleValIleValIleValIleVal 286
 Db 694 ATGTTTATGAGAACTTAAACCAAGAAATATTTGCTAATTCACAGGACACATTTGTC 753
 QY 287 IleThrAspPheGlyLeuCysLysGluGlyIleThrAspAlaAlaThrMetLysThrPhe 306
 Db 754 CTTAATGACTTCCGACTCTGCAAGAGAAACATTGAACACACACACATCCACCTTC 813
 QY 307 CysGlyThrProGluTrpLeuAlaProGluValIleGluLysAsnAspTrpGlyArgAla 326
 Db 814 TGTGGACGCGCGAGATCTCGCACCTGAGGTGCTCATAGACGCTTATGACAGACT 873
 QY 327 ValAspTrpTrpGlyLeuGlyValValMetTrpGluMetCysGlyValGluProPhe 346
 Db 874 GTGAGCTGTGTGGCTCGGAGGCTGCTGTATGAGATGCTGATGAGCTGCGCGCTTTT 933
 QY 347 TyrAsnGluAspHisGlyLysLeuPheGluLeuIleLeuMetGluAspIleLysPhePro 366
 Db 934 TATAGCCGAAACACAGCTGAAATGTACGACACATTTGTGAACAAGCTCTCCAGCTGAA 993
 QY 367 ArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeuLeuIleLysAspProAsn 386
 Db 994 CCAAAATATTACAATTCGCGAAGACACCTCTCGAGGGCTCTCTCGCAGAAAGACAGACA 1053
 QY 387 LysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMetArgHisSerPhePheSer 406
 Db 1054 AAGCGGCTC---GGGCGCAAGATGACTTCATGAGATTAAGAGTCAATGCTTCTTCTTC 1110
 QY 407 GlyValAsnTrpGluAspValIleValAspLysLeuValProPheLysProGlnVal 426
 Db 1111 TTAAATTAACTGGAGTGTCTCATTAATTAAGAGATTACTCCCTTTTAAACCAAAATGTG 1170

QY 427 ThrSerGluThrAspThrArgTrpPheAspGluGluPheThrAlaGlnThrIleThrIle 446
 Db 1171 AGTGGGCCCAACGACCTTACGAGCACTTGAACCCGAGATTATCCGAAAGCCTGTCCCAAC 1230
 QY 447 ThrProGluLysTrpAspGluAspGlyMetAspCysMetAspAsnGluArgPro 466
 Db 1231 TCCATTGGCAAGTCCCTTACAGCCCTCTCTGTCACAGCAGCTCAAGAAAGCTGCCGAG 1290
 QY 467 HisPheProGluPheSerTrpSer 474
 Db 1291 GCTTCTTACGCTTCTTCTTATGCG 1314
 RESULT 14
 US-09-031-295-1
 / Sequence 1, Application US/09031295
 / Patent No. 6326181
 / GENERAL INFORMATION:
 / APPLICANT: LANG, Florian
 / APPLICANT: WALDEGER, Tubingen
 / TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
 / NUMBER OF SEQUENCES: 4
 / CORRESPONDENCE ADDRESSES:
 / ADDRESSEE: FOLEY & LARDNER
 / STREET: 3000 K Street, N.W.
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: U.S.A.
 / ZIP: 20007-5109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent in Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/031,295
 / FILING DATE: 26-FEB-1998
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: DE 197-08-173.8
 / FILING DATE: 28-FEB-1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Sandercock, Colin G.
 / REGISTRATION NUMBER: 31,298
 / REFERENCE/DOCKET NUMBER: 058315/0123
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202) 672-5300
 / TELEFAX: (202) 672-5399
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 2370 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 43..1335
 / US-09-031-295-1
 Alignment Scores:
 Pred. No.: 3,37e-96 Length: 2370
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 Percent Similarity: 61.10% Conservative: 65
 Best Local Similarity: 45.58% Mismatches: 135
 Query Match: 35.54% Indels: 28
 DB: 3 Gaps: 7
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 Db 124 ATGAACAGAGAGAGATGGGTCTGAACGACTTATTACAGAG----- 165


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QY      82 ValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGluAla 101
      166 ATGGCAATTAACCTCTATGATGCAACACCTGAA----- 201
QY      102 IleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSerPro 121
      202 GTTCAGTCCATCTTGAAGATCTCCCAACCTCAGACCTGAGCTTATGTAATGCCAACCTT 261
QY      122 Thr-----SerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSer 136
      262 TCTCTCCCAACCAAGCTCTCTCAGCAATCAACCTTGGC-----CCGTGCTCC 309
QY      137 ThrThrHisIleAspArgLeuThrMetAsnAspPheAspTyrLeuIleuGlyLys 156
      310 AATCCCATGCTTAA-----CCATGCACTTTCCTCTTGAAGATCGGAAG 360
QY      157 GlyThrPheGlyLysValIleLeuValArgGluLysAsnSerGlyLysTyrAlaMet 176
      361 GGCAGTTTGGAAAGGTTCTTCTAGCAAGACACAGGCAAGAGAGTGTCTATGCAAGTC 420
QY      177 LysIleLeuLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlu 196
      421 AAAGTTTACAGAGAAAGCAATCTGAAAAGAAAGAGAGAGATATTATGTCGAG 480
QY      197 SerArgVal---LeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPhe 215
      481 CGGAATGTTCTGTGGAAGATGGAAGCAACCTTCTGTGGGCTTCACTTCTCTTC 540
QY      216 GlnThrLysAspArgLeuLysPheValMetGluTyrValAsnGlyGluLeuPhePhe 235
      541 CAGACGTGCGCAAAATTTGACTTGTCTTCTAGCACTATGATGATGAGAGTGTCTAC 600
QY      236 HisLeuSerArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIle 255
      601 CATCTCCAGAGGAGAGCTGCTCTCGAACCAGCGGCTGTCTATGCTGTGAAATA 660
QY      256 ValSerAlaLeuAspTyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGlu 275
      661 GCCAGTGCCTTGGGCTACCTGCATTCACGCAATGCTTTATGAACTTAAACACAGAG 720
QY      276 AsnLeuMetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlu 295
      721 AATATTTTGTATGATTCACAGGACACATGTTCTCTACTGATTTCCGACTGCAAGAG 780
QY      296 GlyIleThrAspAlaIleAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaPro 315
      781 AACATTGAACACACAGCACACATCCACTTGTGGACGCGGAGATATCTCGACCT 840
QY      316 GluValIleGluLysAspAsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValAla 335
      841 GAGGTCTTCATAGACAGCCTTATGACAGACGTGAGCTGAGTGGCTGGGAGCTGTC 900
QY      336 MetTyrGluMetCysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPhe 355
      901 TTGTATGAGATCTGTATGGCTCGCGCTTTTATAGCAAAACAGCTGAAATGATAC 960
QY      356 GluLeuIleLeuMetGluAspLysIleLysPheProArgThrLeuSerSerAspAlaLysSer 375
      961 GACACATTTCTGAACAGCCTCTCCAGCTGAAACCAATATTTCGAATTCGCAAGACAC 1020
QY      376 LeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyLysGlyProAspAsp 395
      1021 CTCCTGGAGGGCTCTCTGCAAGAGACAGACAAACCGCTC---GGGCGCAAGATGAC 1077
QY      396 AlaLysGluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAsp 415
      1078 TTTCATGAGATTAAGATCATGCTCTCTCTTCTTATTAATGATGATGATCATTAAT 1137
QY      416 LysLysLeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPhe 435
      1138 AAGAGATTACTCCCTTTTAACCAATGTGAGTGGGCCAACGAGCTTACGGCACTTT 1197

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QY      436 AspGluGluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAsp 455
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QY      456 GlyMetAspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSer 474
      1258 CTCGTCACAGCCAGCGCTCAAGAGAGCTGCGAGGCTTCTTGAAGCTTCTTATGCG 1314
DB      1258 CTCGTCACAGCCAGCGCTCAAGAGAGCTGCGAGGCTTCTTGAAGCTTCTTATGCG 1314

RESULT 15
US-08-712-709-6
Sequence 6, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-712-709-6

Alignment Scores:
Pred. No.: 9.55e-96 Length: 2311
Score: 905.00 Matches: 191
Percent Similarity: 60.86% Conservative: 64
Best Local Similarity: 45.58% Mismatches: 136
Query Match: 35.38% Gaps: 28
DB: 2 Gaps: 7

US-09-869-079B-3 (1-479) x US-08-712-709-6 (1-2311)
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      91 ATGAAGCAGAGAGAGTGGCTTGAACGACTTTATTCAGAG- 132
QY      82 ValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGluAla 101
      133 ATGGCAATTAACCTCTATGATGCAACACCTGAA----- 168
QY      102 IleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSerPro 121
      169 GTTCAGTCCATCTTGAAGATCTCCCAACCTCAGAGCTTCACTTATGTAATGCCAACCT 228

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 13, 2005, 08:56:25 ; Search time 688 seconds

(without alignments)
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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-MAXLEN=200000000 -USER=US09869079.@CGN_1_1723@runat_11042005_190025_13497
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Database: Published Applications_NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2558	100.0	2811	15 US-10-324-985A-4	Sequence 4, Appl
2	2558	100.0	2811	19 US-10-753-267-107	Sequence 107, App
3	2402	93.9	1570	10 US-09-526-043-1	Sequence 1, Appl
4	2402	93.9	1570	17 US-10-394-043-1	Sequence 1, Appl
5	2105.5	82.3	2729	19 US-10-895-225A-36	Sequence 36, Appl
6	2105.5	82.3	2978	10 US-09-955-999-43	Sequence 43, Appl
7	2100.5	82.1	2626	18 US-10-324-985A-1	Sequence 1, Appl
8	2100.5	82.1	2626	18 US-10-713-678-5	Sequence 5, Appl
9	2100.5	82.1	2626	19 US-10-735-461-20	Sequence 20, Appl
10	2100.5	82.1	2626	19 US-10-895-225A-56	Sequence 56, Appl
11	2099.5	82.1	2181	14 US-10-072-036-70	Sequence 70, Appl
12	2099.5	82.1	2184	14 US-10-072-036-138	Sequence 138, App
13	2099.5	82.1	2610	9 US-09-970-000-3	Sequence 3, Appl
14	2099.5	82.1	2610	17 US-10-388-263-339	Sequence 329, Appl
15	2099.5	82.1	2610	17 US-10-641-643-1206	Sequence 1206, App
16	2099.5	82.1	2610	18 US-10-713-678-1	Sequence 1, Appl
17	2099.5	82.1	2610	18 US-10-735-461-22	Sequence 22, Appl
18	2099.5	82.1	2610	19 US-10-823-433-3	Sequence 3, Appl
19	2004	78.3	1599	15 US-10-324-985A-3	Sequence 3, Appl
20	2004	78.3	1599	15 US-10-641-643-1004	Sequence 254, App
21	2004	78.3	1715	15 US-10-007-926A-354	Sequence 254, App
22	2004	78.3	1715	19 US-10-735-461-23	Sequence 23, Appl
23	2004	78.3	2562	18 US-10-322-281-415	Sequence 415, App
24	1998	78.1	1722	18 US-10-322-281-412	Sequence 412, App
25	1998	78.1	1741	15 US-10-324-985A-2	Sequence 2, Appl
26	1998	78.1	1741	19 US-10-735-461-21	Sequence 21, Appl
27	1998	78.1	3010	19 US-10-895-225A-57	Sequence 57, Appl
28	1798.5	70.3	1254	18 US-10-713-678-3	Sequence 3, Appl
29	1641.5	64.2	3712	18 US-10-473-939-7	Sequence 7, Appl
30	1637	64.0	1140	15 US-10-324-985A-5	Sequence 5, Appl
31	1511.5	59.1	1854	14 US-10-198-846-9984	Sequence 9984, Ap
32	1334	52.2	2410	9 US-09-771-161A-66	Sequence 66, Appl
33	1236	48.3	879	17 US-10-424-599-21419	Sequence 21419, A
34	992	38.8	968	9 US-09-771-161A-65	Sequence 65, Appl
35	960	37.5	758	9 US-09-910-943-677	Sequence 677, App
36	949.5	37.1	1335	17 US-10-116-275-285	Sequence 285, App
37	916	35.8	1338	16 US-10-067-977-1	Sequence 1, Appl
38	916	35.8	1338	18 US-10-827-272-1	Sequence 1, Appl
39	914.5	35.8	3196	17 US-10-094-749-222	Sequence 222, App
40	913	35.7	1315	17 US-10-403-161-3	Sequence 3, Appl
41	913	35.7	2343	17 US-10-403-161-1	Sequence 1, Appl
42	913	35.7	2354	16 US-10-210-120-22	Sequence 22, Appl
43	913	35.7	2365	9 US-09-981-353-6	Sequence 6, Appl
44	909	35.5	2370	9 US-09-969-347-214	Sequence 214, App
45	909	35.5	2370	9 US-09-880-107-3855	Sequence 3855, Ap

ALIGNMENTS

RESULT 1
US-10-324-985A-4
Sequence 4, Application US/10324985A
Publication No. US20030144204A1
GENERAL INFORMATION:
APPLICANT: Spencer, David
TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REFERENCE: P022480S1/10106761
CURRENT APPLICATION NUMBER: US/10/324,985A
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,155
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2811
TYPE: DNA
ORGANISM: human
US-10-324-985A-4

Alignment Scores:

Pred. No.: 6,866-280 Length: 2811
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-869-079B-3 (1-479) X US-10-324-985A-4 (1-2811)

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QY 1 MetSerAspValThrIleValIlysgIuGIYTPValGlnIlyAspGlyIuGIYrIleIys 20
DB 1 ATGAGGAGATGTTACCAATTGGAAAGAGGTGGGTTCAAGAGAGGAGATATATAA 60
QY 21 AsnTrpArgProArgTrpPheLeuLeuIlyThrAspGlySerPheIleGIYrIlysgIu 40
DB 61 AACTGGAGGCGAAGATGATCTCTTTGAAAGACAGATGGCTCATTCATAGGATATAAGAG 120
QY 41 LysProGlnAspValAspLeuProIYrProLeuAsnAspPheSerValAlalysCysGln 60
DB 121 AAACCTCAAGATGGATTTTACCTTATCCCTCAACACATTTTCAATGGCAAAATGCCAG 180
QY 61 LeuMetIlyThrGluArgProIlyProAsnTrpPheIleIleArgCysLeuGlnTrpTr 80
DB 181 TTAAATGAAAACAAAGACCAAGCCAAACACATTTATATATCATGATGTCTCCAGTGGACT 240
QY 81 ThrValIleGluArgTrpPheIleValAspTrpProGluGluArgGluIuTrpTrGlu 100
DB 241 ACTGTTATAGAGAAACATTTCTATGATGATCTCCAGAGAAAGGAAAGATGACAGAA 300
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgIuGluIuArgMetAspCysSer 120
DB 301 GCTATCCAGGCTGTAGACAGACACTGCAGAGCAAGAGAGAGAGAGATGATTTGATG 360
QY 121 ProTrpSerGlnIleAspAsnIleGIYrIlyGluGluMetAspAlaSerThrTrpHis 140
DB 361 CCAACTCTCAAAATTTATATATATAGAGAGAGAAAGATGATGCTCTCAACCCATCAT 420
QY 141 LysArgIlyThrMetAspAspPheAspTrpLeuIlyLeuLeuGIYrIlysgIyThrPheGly 160
DB 421 AAAAGAAAGCAATGATGATTTTGATTTGATTTAACTATAGATTAAGGCACTTTGGG 480
QY 161 LysValIleLeuValArgIuIyValAspGlyLysTrpTrpAlaMetLysIleLeuLys 180
DB 481 AAAGTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCATCTATGAAGATTCGAGAG 540
QY 181 LysGluValIleIleIleAlaLysAspGluValAlaHisIleThrLeuThrGlnSerArgValIle 200
DB 541 AAAAGAGTCATTAATTCGAAAGATGAGTGGCAACACACTCTAATAAGCCAGATATTA 600
QY 201 LysAsnTrpArgHisProPheLeuTrpSerLeuIlyTrpSerPheGlnTrpLysAspArg 220
DB 601 AAGAACATCATGACATCCCTTTTAAACATCTCTGAATATCTCTCCAGACAAAGACCGT 660
QY 221 LeuCysPheValMetIuTrpValaAsnGIYrIlyGluLeuPhePheHisIleuSerArgIu 240
DB 661 TTGTGTTTGTGATGGAATATGTTATGGGGGAGACTGTTTTTCCATTTGTGACAGAG 720
QY 241 ArgValIlePheSerGluAspArgTrpArgPheTrpGlyAlaGluIleValSerAlaLeuAsp 260
DB 721 CCGGTGTTCTCTGAGAGACCGCAACGTTTCTAAGTGGAGAAATTCCTCTGCTGCTGAGC 780
QY 261 TyrLeuHisSerGlyLysIleValIYrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 781 TATCTCATTTCCGAAAGATGTGATCCGATGCTCAAGTTGAGAAATCTTAATGCTGGAGC 840
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysIlysgIuGIYrIleThrAspAla 300
DB 841 AAAGATGGCCACATAAAATTAAGATTTTGGACTTTGGCAAAAGAGATCAAGATGCA 900
QY 301 AlaThrMetLysThrPheCysGlyTrpProGluTrpLeuAlaProGluValLeuGluAsp 320
DB 901 GCCACATGAAAGCATTTGTGTGACACTCCAGAAATATCTGGCAAGAGGTTAGAAAGAT 960

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QY 321 AsnAspTrpArgIYrArgAlaValAspTrpTrpGlyLeuGluIYrValMetTrpGluMetMet 340
DB 961 AATGACTATGGCCGAGACATGATCTGTGGGCTTCAAGATGATGATGATGATGATG 1020
QY 341 CysGlyArgLeuProPheTrpAsnGlnAspHisIleGluLysLeuPheGluLeuIleuMet 360
DB 1021 TGTGGAGGTTACCTTCTTACAAACGAGACATGAGAAACCTTTTGAATTAATATTAAG 1080
QY 361 GluAspIleLysPheProArgTrpTrpLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1081 GAAGACATTAATTTCTCGAAACACTCTCTTCAAGATGCAAAATCATTTGCTTACAGGGCTC 1140
QY 381 LeuIleLysAspProAsnLysArgLeuGIYrIlyGlyProAspAspAlaLysGluIleMet 400
DB 1141 TTGATTAAGATTCCAATTAACGCTTGTGAGAGACCAAGATGACAAAGAAATTAATG 1200
QY 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValIYrAspLysLysLeuValPro 420
DB 1201 AGACACAGTTCTTCTCTGAGTAAACCTGCAAGATGATATGATTAAGTGTGACCT 1260
QY 421 ProPheLysProGlnValIleThrSerGluTrpAspTrpArgTrpPheAspGluIuPheThr 440
DB 1261 CCTTTAAACCTCAAGTAACTGAGACATCTGAGACATCAATTTGATGATGAAGATTTTACA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluIyTrpAspGluAspGlyMetAspCysMet 460
DB 1321 GCTCAGACATTTTCAATTAACACCACTGAAATATGATGAGATGATGATGATGATG 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTrpSerAlaSerGlyArgGlu 479
DB 1381 GACAATGAGAGCGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGAAGAGAA 1437

RESULT 2
US-10-753-267-107
; Sequence 107, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stegiano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodrigue-May, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33566, 53656, 44443, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; FILE REFERENCE: MP103-003PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414

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; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1440)
US-10-753-267-107

Alignment Scores:
Pred. No.:      6,86e-280      length:      2811
Score:          2558.00      Matches:      479
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              19          Gaps:      0

US-09-869-079B-3 (1-479) x US-10-753-267-107 (1-2811)

QY      1 MetSerAspValThrIleValLyrgluGlyTrpValGlnLysArgGlyIuTyrlleLys 20
DB      1 ATGAGCGATGTTACATTTGTAAGAAAGGTTGGGTTGAGAAAGGGGAGATATATATTA 60
QY      21 AsnTPArProArgTrpPheLeuLeuLysThrAspGlySerPheIleGlyTyrlLysGlu 40
DB      61 AACTGAGGCGCAAGATACCTCTTTGGAACAGATGCTCATTCATAGATATAAGAG 120
QY      41 LySProGlnAspValAspLeuProGlyProLeuAsnAspPheSerValAlaLysCysGln 60
DB      121 AAACCTCAGATGTTGATTTTACCTTATCCCTCAACACTTTTCAAGGCAAAATGCCAG 180
QY      61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
DB      181 TTATGTAAGAACAGACAGACCAAGCCAAACACATTTATATCAAGATGCTCCAGTGACT 240
QY      81 ThrValIleGluArgThrPheIleValAspThrProGluGluArgGluIuTrpThrGlu 100
DB      241 ACCTGATATAGAGAAACATTTCAATGATATCTCCAGAGAAAGGGAAGATGACAGAA 300
QY      101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluIuArgMetLysCysSer 120
DB      301 GCTATCCAGGCTTAGCAGACAGACTGCAAGGCGAAGAGAGAGAGATGAATGTAGT 360
QY      121 ProThrSerGlnIleAspAsnIleGlyGluGluIuMetAspAlaSerThrTrhIshIs 140
DB      361 CCAACTTCAAAATTTGATATATAGGAGAGAGATGATGCTCTTCAACCCATCAT 420
QY      141 LySArgLysThrMetLysAspPheAspTyrlLysLeuLeuGluGlyLysGlyThrPheGly 160
DB      421 AAAAGAAAGCAATGATGATTTTGACTATTTGAAACTACTAGATAAGGACACTTTGGG 480
QY      161 LySValIleLeuValArgGluLysAlaSerGlyLysTyrlLysIleMetLysIleLeuLys 180
DB      481 AAAGTTATTTTGGTTGAGAGAGGCAAGTGAGAAATATCATGCTATAGAAATCTGAG 540
QY      181 LySgluValIleIleAlaLysAspGluValAlaIshIleThrLeuThrGluSerArgValLeu 200
DB      541 AAAGAAGTCAATTTAGGAAAGATGAAGTGACACACTTAACTGAAACAGAGATTA 600
QY      201 LySAsnThrArgHisProPheLeuThrSerLeuLysTyrlSerPheGlnThrLysAspArg 220
DB      601 AAAGAACATGAGATCCCTTTTAAACATCTTGAATAATATCTTCCAGCAAAAGACCGT 660
QY      221 LeuCyPheValMetGluTyrlValLeuGlyGlyIuLeuPhePheHisLeuSerArgGlu 240
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DB      661 TTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCCATTTGTGAGAGAG 720
QY      241 ArgValPheSerGluAspArgThrArgPheTyrlValAlaGluIleValSerAlaLeuAsp 260
DB      721 CGGGTGTCTCTGAGGACCGCACACCTTTCTAATGAGGCAAGAAATTTCTCTGCTTGAC 780
QY      261 TyrlLeuHisSerGlyLysIleValTyrlArgAspLeuLysLeuGluLysIleLeuMetLysAsp 280
DB      781 TATCTACATTCGAGAAAGATGTGTACCGGATCTCAAGTGTGAGAAATCTTAATGCTGGAC 840
QY      281 LySAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
DB      841 AAAGATGCGCACATTAATAATTTACAGATTTTGGACTTTGCAAAAGAGATCAAGATGCA 900
QY      301 AlaThrMetLysThrPheCysGlyThrProGluTyrlLeuAlaProGluValLeuGluAsp 320
DB      901 GCCACCATGAAAGCATTTCTGTGCACTCCAGATATCTGACACAGAGGTTTGAAGAAGT 960
QY      321 AsnAspTyrlValArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrlMetMet 340
DB      961 AATGACTATGGCCGACAGACAGACTGCTGGGCTTGAAGGCTGTCAATGTAAGATGATG 1020
QY      341 CysGlyArgLeuProPheTyrlAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
DB      1021 TGTGGAGGTTACCTTTCTACAAACAGACAGACATGAAACTTTTGATTAATTAATG 1080
QY      361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB      1081 GAAGACATTAATTTCTCTGCAACACTCTCTTCAGATGCAAAATCATTTGTCAGGGCTC 1140
QY      381 LeuIleLysAspProAsnLysArgLeuGlyGlyIuProAspAspAlaLysGluIleMet 400
DB      1141 TTGATTAAGAGATCAATTAACCCCTTGGAGAGACAGATGATCAAAAGAAATTAAG 1200
QY      401 ArgHisSerPhePheSerGlyValAsnTPGlnAspValTyrlAspLysLysLeuValPro 420
DB      1201 AGACACAGTTTCTTCTCTGAGATTAACCTGCAAGATGTAATGATTAAGATTTTACA 1260
QY      421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrlPheAspGluIuPheThr 440
DB      1261 CTTTAAACCTCAATTAACATCTGACAGACAGATCAATATTTGATGAAAGATTTTACA 1320
QY      441 AlaGlnThrIleThrIleThrProProGluLysTyrlAspGluAspGlyMetAspCysMet 460
DB      1321 GCTCAGACTAATTAACAATAACACCACTGAAAAATATGAGAGATGTAAGCTGCATG 1380
QY      461 AspAsnGluArgArgProHisPheProGlnPheSerTyrlSerAlaSerGlyArgGlu 479
DB      1381 GACATGAGAGGCGCGCATTTTCTCTCAATTTTCTTACTCTGCAAGTGACAGAA 1437

RESULT 3
US-09-526-043-1
; Sequence 1, Application US/09526043
; Publication No. US20030100049A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagmont, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; EARLIER FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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LOCATION: (126) ..(1523)
US-09-526-043-1

Alignment Scores:

Pred. No.:	1,61e-262	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	10	Gaps:	1

US-09-869-079B-3 (1-479) x US-09-526-043-1 (1-1570)

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QY 1 MetSerAspValThrIleValIysGluGlyTPVAlGlnIleYserGlyIuTrIleYs 20
DB 126 ATGAGCGAGTTCACCTTGTGAAGAAGTTGGTTCCAGAAAGGGGAGAAATATATAA 185
QY 21 AsnTPArGProArGTYrPheLeuLeuIysThrAspGlySerPheIleGlyTYrIysGlu 40
DB 186 AACTGAGGCGCAAGATATCTCTTTGAAGACAGATGGCTCATTCATGATATAAAG 245
QY 41 LysProGlnAspValAspLeuProTYrProLeuAsnAspPheSerValAlaIysCysGln 60
DB 246 AAACCTCAAGATGTGATTTACTTATCCCTCAACACTTTTCAGTGGCAAAATGCCAG 305
QY 61 LeuMetIysThrGluArgProIysProAsnThrPheIleIleArgCysLeuGlnTPThr 80
DB 306 TTTATATAAACAAGACAGCAACCAAGCAACATTTATATCATGATCTCCAGTGGACT 365
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTPThrGlu 100
DB 366 ACTGTTATAGAGAAACATTTTCATGTAGATACCTCAGAGAAAGGAGAAATGACAGAA 425
QY 101 AlaIleGlnAlaValIleAspArgLeuGlnArgGluGluArgMetAsnCysSer 120
DB 426 GCTATCAGAGCTGTACAGACACTGCAGAGCAAGAGAGAGAAATGAAATTTAGT 485
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 140
DB 486 CCAACTTCACAAATTGATATATATAGAGAGAGAAATGATGCTCTCAACACCATCAT 545
QY 141 LysArgIysThrMetAsnAspPheAspTYrLeuIysLeuLeuGlyIysGlyTYrPheGly 160
DB 546 AAAAGAAACAATGATGATGATTTGACTATTTGAAACTACTAGATAAAGGCACTTTGG 605
QY 161 LysValIleLeuValArgIuIysAlaSerGlyIysTYrTYrAlaMetIysIleLeuIys 180
DB 606 AAAGTATTTTGGTTGAGAGAAAGCAAGTGGAAATACTATGCTATGAAAGATTCGAAG 665
QY 181 LysGluValIleIleAlaIysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 666 AAAGAAATCATTTATTCAGAAAGATGAGATGGCAACACTCTAATAAGCAAGATATTA 725
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuIysTYrSerPheGlnThrIysAspArg 220
DB 726 AAGAAACATAGACATCTTTTAAACATCTTGAAATATTTCTCCAGCAAAAGACCGT 785
QY 221 LeuCysPheValMetGluTYrValaAsnGlyIysGluLeuPheHisIleuSerArgGlu 240
DB 786 TTGTGTTTGTGATGAAATATGTTAAATGGGGGCACTGTTTTCATTTGTGAGAGAG 845
QY 241 ArgValPheSerGluAspArgThrArgPheTYrGlyAlaGluIleValSerAlaLeuAsp 260
DB 846 CCGGCTTCTCTGAGAGACCGCAACGTTTCTATGCGTGAAGAAATTTCTCTGCTGGAC 905
QY 261 TYrLeuHisSerGlyIysIleValIYrArgAspLeuIysLeuGluAsnLeuMetLeuAsp 280
DB 906 TATCTCATATCCGGAAGATTTGTGACCGGTGATCTCAAGTTGAGAGATCTAATGCTGAG 965
QY 281 LysAspGlyIleIleIysIleThrAspPheGlyLeuCysIysGluGlyIleThrAspAla 300
DB 966 AAAGATGGCCACATAAAATTAACAATTTTGACTTTGCAAAAGAGGATCAACAGATGCA 1025

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QY 301 AlaThrMetIysThrPheCysGlyTYrProGluTYrLeuAlaProGluValLeuGluAsp 320
DB 1026 GCCACCATGAAACATTTCTGTGGCACTCCAGAAATATCTGGACACAGAGGTATTAGAAAT 1085
QY 321 AsnAspTYrGlyIysArgAlaValAspTPTrPTrGlyLeuGlyValIleMetTYrGluMet 340
DB 1086 AATGACTAATGGCGGAGCAGATACCTGTGGGGCTTGAAGGGTGTGATGTATGAAATGATG 1145
QY 341 CysGlyIysGluProPheTYrAsnGlnAspHisGlyIysLeuPheGluLeuIleuMet 360
DB 1146 TGTGGAGGTTACCTTTCTTACACCAAGACCATGAGAACTTTTGAATTAATTAATG 1205
QY 361 GluAspIleIysPheProArgThrLeuSerSerAspAlaIysSerLeuLeuSerGlyLeu 380
DB 1206 GAAAGCATTAATTTCTTCGAAACATCTCTTCAGATGCAAAATCATTTGTTCAAGGGCTC 1265
QY 381 LeuIleIysAspProAsnIysArgLeuGlyIysGlyProAspAspAlaIysGluIleMet 400
DB 1266 TTGATTAAGATCCAAATMAAGCCTTGTGTGAGACCAAGATGACAAAGAAATTATG 1325
QY 401 ArgHisSerPhePheSerGlyValAsnTPGlnAspValTYrAspLysIleuValPro 420
DB 1326 AGACACATTTCTTCTGTGAGTAACTGGCAAGATGATATGATATAAAGCTTGACTCT 1385
QY 421 ProPheIysProGlnValThrSerGluThrAspThrArgTYrPheAspGluGluPheThr 440
DB 1386 CTTTTTAAACCTCAAGTAAACATCTGAGACAGATACATGATTTTGATGAAGATTTACA 1445
QY 441 AlaGlnThrIleThrIleThrProProGluIysTYrAspGluAspGlyMetAspCys 459
DB 1446 GCTCAGACTATTAACAATAACACCACTGAAATATGTCAAGCAATCA-----GATTGT 1496

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RESULT 4

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US-10-394-568-1
; Sequence 1, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUN, KUN
; APPLICANT: IVASHCHENKO, YURI
; APPLICANT: CLARK, KENNETH L.
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; FILE REFERENCE: A33990
; CURRENT APPLICATION NUMBER: US/10/394,568
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126) ..(1523)
US-10-394-568-1

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Alignment Scores:

Pred. No.:	1,61e-262	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	17	Gaps:	1

US-09-869-079B-3 (1-479) x US-10-394-568-1 (1-1570)

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QY 1 MetSerAspValThrIleValIysGluGlyTPVAlGlnIleYserGlyIuTrIleYs 20
DB 126 ATGAGCGAGTTCACCTTGTGAAGAAGTTGGTTCCAGAAAGGGGAGAAATATATAA 185
QY 21 AsnTPArGProArGTYrPheLeuLeuIysThrAspGlySerPheIleGlyTYrIysGlu 40

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186 AACGGAGGCGCAAGATCTCTTTTGAAGACAGATGGCTCATTCATAGGATATTAAG 245
41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheserValAlaLysCysGln 60
246 AAACCTCAAGATGGATTTTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCGAG 305
61 LeuMetLysThrGluArgProLysProAsnThrPheLeilethArgCysLeuGlnTyrThr 80
306 TTATGAAAGACAGACCAAGCCAAAGCCAAACATTATTAATCAGATCTCTCCAGTGGACT 365
81 ThrValilegIuArgThrPheHisValAspThrProGlnGluArgGlnGluTyrThrGlu 100
366 ACTGTTATAGAGAAATTCATTTCATGTGATATCTCCAGAGAAAGGAAAGATGACAGAA 425
101 AlailegIuAlaValAlaAspArgLeuGlnArgGlnGlnGluGluArgMetAsnCysSer 120
426 GCTATCCAGGCTGTAGCAGACAGCTGCAGAGGCAAGAGAGAGAGAAATGAATTGTAGT 485
121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHisHis 140
486 CCAACTTCACAAATGTGATATATAGAGAGAGAGAGATGATGCTCTTACACCCATCAT 545
141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuGlnGlyLysGlyThrPheGly 160
546 AAAAGAAAGCAATGATGATTTGACTATTTGAAACTAGGTAAAGGACATTTTGGG 605
161 LysValileuValAlaArgIuLysValAspGlyLysGlyTyrAlaMetLysileuLys 180
606 AAAGTTATTTTGGTTCGAGAGAAAGGCAAGTGAATAATCATGCTATGAGATTCAGAG 665
181 LysGluValIleleuLysAspGluValAlaHisPheThrLeuThrGluSerArgValLeu 200
666 AAAGAACTCATATGTGCAAGAGATGAAGTGCACACACTGAACCTGAACCAAGATTTA 725
201 LysAsnThrArgHisPheProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
726 AAGAACACTAGACATCCCTTTTAAACATCCTTGAAATATCTCTCCAGACAAAAGACCT 785
221 LeuCysPheValMetCyluTyrValAsnGlyGlyLeuPhePheHisLeuSerArgGlu 240
786 TTGTGTTTGTGATGGAATGTGTTAATGGGGGCGAGCTGTTTCCATTTGTGAGAGAG 845
241 ArgValPheSerGluAspArgThrArgPheTyrGlyValAsnIleValIleSerAlaLeuAsp 260
846 CGGATGTTCTCTAGAGACCGCACACGTTTATGTGTCACAAATTTGCTGTGCTTGAC 905
261 TyrLeuHisSerGlyLysIleValIleTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
906 TATCTACATTCGCGAAAGATTTGTGTACCGGTGATCTCAAGTTGGAAGATCTAAATGCTG 965
281 LysAspGlyHisIleLysIleThrAspPheGlyLeuGlyLysGlyGlyIleThrAspAla 300
966 AAAGATGGCCACATAAAAAATTACGATTTTGGACTTTGCAAGAGGATCACAGATGCA 1025
301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValIleLeuGluAsp 320
1026 GCCACCATGAAAGCATTTCTGTGCACTCCAGAAATATCTGCAACAGAGGCTGTAGAGAT 1085
321 AsnAspTyrGlyValArgAlaValAspTyrPyrGlyLeuGlyValValMetTyrGluMetMet 340
1086 AATGATCTATGGCCGAGACAGTACGTGTGGGGCTTACGGGCTGTGATGTAAGATGATG 1145
341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
1146 TGTGGAGGTTTACTTTCTCAACACAGGACCATGAGAACTTTTGAATTAATTAATGATG 1205
361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
1206 GAAGACATTAATTTCTTCAGACATCTTTCAGATGCAAAATCATTTGAGGGCTC 1265
381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400

1266 TTGATTAAGGATCCAAATAAGCGCTTGGTGAGAGCCAGATGATGCAAAAGAAATTAATG 1325
401 ArgHisSerPhePheSerGlyValAsnTyrPyrGlnAspValTyrAspLysLeuValPro 420
1326 AGACACAGATTTCTTCTCTGAGATGAACCTGGCAAGATGATATATATAAAGCTGTACCT 1385
421 ProPheLysProGlnValThrSerGluTyrAspThrArgTyrPheAspGluGluPheThr 440
1386 CTTTAAACCTCAAGTAAATCTGAGACAGATCTAGATATTTTGTATGAAAGATTTTACA 1445
441 AlaGlnThrIleThrIleThrProProGluTyrTyrAspGluAspGlyMetAspCys 459
1446 GCTCAGCTATTAATTAATACACACCTGAAAAATGTACAGAAATCA-----GATTGT 1496

RESULT 5
US-10-895-225A-36
Sequence 36, Application US/10895225A
Publication No. US20050048587A1
GENERAL INFORMATION:
APPLICANT: Rao, Patricia
APPLICANT: Snyder, Jessica
APPLICANT: Bagley, Andria
TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
FILE REFERENCE: TUN-025
CURRENT APPLICATION NUMBER: US/10/895,225A
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/488,502
PRIOR FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 161
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 2729
TYPE: DNA
ORGANISM: Homo sapiens
US-10-895-225A-36

Alignment Scores:
Pred. No.: 1,966-228 Length: 2729
Score: 2105.50 Matches: 397
Percent Similarity: 90.21% Conservative: 36
Best Local Similarity: 82.71% Mismatches: 42
Query Match: 82.31% Indels: 5
DB: 19 Gaps: 4

US-09-869-079B-3 (1-479) x US-10-895-225A-36 (1-2729)

1 MetSerAspValThrIleValLysGluGlyTyrPyrValGluLysArgGlyGlyTyrIleLys 20
276 ATAGCGACGTGGCTATTTGTAGAGAGGTTGGCTCACAACAGAGGGAGTACATCAAG 335
21 AsnTyrPyrProArgTyrPheLeuLeuLysAspGlySerPheIleGlyTyrLysGlu 40
336 ACTGGCGGCGACAGCTACTTCCCTCAAGAAATGATGGACCTTATTTGGCTTCAAGAG 395
41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheserValAlaLysCys 59
396 CGGCCCAAGATGTGACCAACGTAGAGCTCCCTCCCAACACTTCTGTGGCGCAGTGC 455
60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIlelethArgCysLeuGlnTyr 79
456 CAGCTATGAAAGCGAGGGGCGCCGCGCCCAACACCTTATCATTCGCTGCGCAGTGG 515
80 ThrThrValilegIuArgThrPheHisValAspThrProGluGluArgGlnGluTyrThr 99
516 ACCACTGTATGAGAGGACCTTTCATGTGAGACCTCTGAGGAGGGGAGGATGAGACA 575
100 GluAlailegIuAlaValAlaAspArgLeuGlnArgGlnGlnGluGluArgMetAsnCys 119
576 ACCGCGATCAAGCTGTGCTGCTGCAAGGCTCAAGAAACAGAGAGAGAGATGAGACTTC 635
120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 139

636 CGGTGGGCTCAACCCAGTGAACAATCAGGGCTGAAGAGATGAGGTCTCCCTGGCCAG 695
140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLysGlyThr 158
696 CCCAAGACCCGGGTGACCAATGAACGATTGATCTTAAGTGTGTGGCAAGGGCACT 755
159 PheGlyLysValIleLeuValArgGlyLysAlaSerGlyLysTyrTrpAlaMetLysIle 178
756 TTCGCAAGATGATCTCTGTGAAGGAAGGACCAAGCGCGCTACTACCCATGAAGATC 815
179 LeuLysLysGlyValIleIleAlaLysAspGlyValAlaHisThrLeuThrGlySerArg 198
816 CTCAGAGAGAAATCTCTGTGGCCAAAGACGAGGTGGCCCACTCACTCCAGAAACCCG 875
199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
876 GTCTGCAAACTCCAGGCAACCCCTTCTCAAGCCCTGAAGTACTCTTCCAGACCTGC 935
219 AsparGlyLeuCysePheValMetGlyTyrValAsnGlyGlyLysLeuPhePheHisLeuSer 238
936 GACCGCTCTGCTTGTCTCATGAGTACGGCAACGGGGGAGAGCTGTTCTTCCACCTGTCC 995
239 ArgGlyLysValPheSerGlyLysAspArgThrArgPheTyrGlyValAlaGlyIleValSerAla 258
996 CGGAGCGGTGTCTCTCCAGAGACCGGGCCGCTTCTATGTGGCTGAGATTGTGTCAAGCC 1055
259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuLysLeu 277
1056 CTGGAATCTCTGACTCGAGAAAGACGTGTGTACGGGACCTCAAGCTGGAGAACCTTC 1115
278 MetLeuAspLysAspGlyLysIleLysIleThrAspPheGlyLysCyseLysGlyLysIle 297
1116 ATGCTGGAACAAGGACGGGACATTAAGATCAACAAGCTTGGGGGTGTGAAGAGGGGATC 1175
298 ThrAspAlaAlaThrMetLysThrPheCyseGlyThrProGlyLysLeuAlaProGlyVal 317
1176 AAGGACGGTGCCACCAATGAAGACCTTTTCCGGCACCTGAGTACCTGGCCCCCGAGGTG 1235
318 LeuGlyLysAspAspArgTyrArgAlaValAspTrpTrpGlyLeuGlyValValMetTyr 337
1236 CTGGAGCAACAATGACTACGGCCGTGCAATGAGTGTGGGGGCTGGGGCTGTGATGTAC 1295
338 GluMetMetCyseGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGlyLeu 357
1296 GAGATGATGTGGGTGTGCTGCTGCTCTCAACACAGAACCAATGAGAACTTTTGTAGCTC 1355
358 IleLeuMetGlyLysIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
1356 ATCTCATGAGAGATCGCTTCCGCGCACCGCTTGTCCGAGGGCCAAAGTCTTGTCTT 1415
378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
1416 TCAAGGCTGTCAAGAAAGACCCCAAGAGCTTGGGGGGCTCCAGAGACGCAAG 1475
398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrArgLysLys 417
1476 GAGATCATGACAGATGCTTCTTTCGCGATATGCTGTGGACAGCACTGTACAGAAAGAG 1535
418 LeuValProProPheLysProGlnValThrSerGlnThrAspThrArgTyrPheAspGly 437
1536 CTCAGCCCAACCTTCAAGCCCGGAGTCAAGTCCGAGACTGACACCGGATTTTGTATGAG 1595
438 GluPheThrAlaGlnThrIleThrIleThrProProGlyLysTyrAspGlyLysMet 457
1596 GAGTTACGGCCCAAGTATGATCACTACATCAACAACCTGACCA-----GATGACAGCAAG 1649
458 AspCyseMetAspAsnGlyLysArgProHisPheProGlnPheSerTyrSerAlaSerGly 477
1650 GAGTGTGTGACAGCAGAGCGGACGCTTCCCAAGTTCCTTCTACTCGGCAAGCGG 1709

RESULT 6
US-09-955-999-43
; Sequence 43, Application US/09955999

Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
; TITLE OF INVENTION: Antibodies, and Methods Based Thereon
; FILE REFERENCE: PT086P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/234,997
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 2978
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2947)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2973)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-955-999-43
Alignment Scores:
Pred. No.: 2,236-228 Length: 2978
Score: 2105.50 Matches: 397
Percent Similarity: 90.21% Conservative: 36
Best Local Similarity: 82.71% Mismatches: 42
Query Match: 82.31% Indels: 5
DB: 10 Gaps: 4
US-09-869-079B-3 (1-479) x US-09-955-999-43 (1-2978)
1 MetSerAspValThrIleValLysGlyLysTyrValGlnLysArgGlyLysGlyLys 20
491 ATGAGCGAGTGTGCTATTGTGAAGAGGTTGGCTGCACAAACGAGGAGTACATCAG 550
21 AsnTrpArgProArgTyrPheLeuLeuLysTyrAspGlySerPheIleGlyTyrLysGly 40
551 ACCGTGGCGGCAACGCTACTCTCTCAAGATGATGAGCACTTATGCTTACCAAGAG 610
41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCyse 59
611 CGGCGGAGAGATGTGACCAACGTGAGGCTCCCTCAACACACTTCTGTGTGGCAGTGC 670
60 GluLeuMetLysThrGlyLysProLysProAsnThrPheIleIleArgCyseLeuGlnTrp 79
671 CAGCTGATGAAGACGAGGCGCCGCGCCCAACACTTATCATATCGCTTGCAGTGG 730
80 ThrThrValIleGlnLysArgThrPheHisValAspThrProGlyLysArgGlyLysTrpThr 99
731 ACCACGTATGAAACGACCTTCCATGTGAGACCTCGAGAGAGCGGAGAGTGGACA 790
100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlyLysArgMetLysCyse 119
791 ACCGCGATCCACACATGTGGCTTCAAGCCCTCAAGAGCAGAGAGAGAGATGAGCTTC 850
120 SerProThrSerGlnIleAspAsnIleGlyGlyLysGlyLysMetAspAlaSerThrThrHis 139
851 CGGTGGGCTCAACCAAGTACCACTCAGGGGCTGAAGAGATGAGGTCTCCCTGGCCAG 910
140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLysGlyLysThr 158
911 CCCAAGACCCGGGTGACCAATGAACGATTGATCTTAAGTGTGTGGCAAGGGCACT 970
159 PheGlyLysValIleLeuValArgGlyLysAlaSerGlyLysTyrTrpAlaMetLysIle 178
971 TTCGCAAGATGATCTCTGTGAAGGAAGGACCAAGCGCGCTACTACCCATGAAGATC 1030

OY	179	LeuValylSGIuValIleIleIleAlaIleValAspGIuValIleIleThrLeuThrGluSerArg	198
Db	1031	CTCAAGAAAGAAATGATGTGGTGGCCAAAGACAGAGTGGGCCCAACACTACCTACCGAAGAACCGC	1090
OY	199	ValIleuValAspThrArgHisProPheLeuThrSerLeuValTyrSerPheGlnThrTys	218
Db	1091	GTCCCTGACAACTCCAGGACACCCCTCTCTCACAGCCCTGAAGTACTCTTTCACAGCCAC	1156
OY	219	AspArgLeuCysPheValMetGluTyrValAsnGlyGlyGluLeuPheHisIleuSer	238
Db	1151	GACCCCTCTCTGCTTGTGATGAGTAAACCCAAACGGGGCGAGCTGTTCTTCCACTGTC	1210
OY	239	ArgGIuArgValPheSerGIuAspArgThrArgPheTyrArgIleValSerIle	258
Db	1211	CGGAGCGGTGTCTTCGAGGACCGGGGCCCTTCTATGGCGCTGAATGTGTCAACC	1270
OY	259	LeuAspTyrLeuHisSerGIlyIys--IleValTyrArgAspLeuValLeuGIuAsnLeu	277
Db	1271	CTGGACTACCTGCACTCGGAGAAAGACGTGGTATCCGGGACTCAACTGGAAGACCTC	1330
OY	278	MetLeuAspTyrAspGIlyHisIleIysIleThrAspPheGIlyLeuCysValGlyGlyIle	297
Db	1331	ATGCTGGACAAGGACGGGCACTTAAAGATCAAGACTTCGGGCTGTGCAGAAAGAGGGATC	1390
OY	298	ThrAspAlaAlaThrMetLeuThrPheCysGIlyThrProGIuTyrLeuAlaProGIuVal	317
Db	1331	AAGACGGTGCACCATGAAGACCTTTGGCGCACACTGAGTACTGGCCCCGAGGTG	1456
OY	318	LeuGIuAspAsnAspTyrGIlyArgAlaValAspTyrTPGIlyLeuGIlyValIleMetTyr	337
Db	1451	CTGGAGGACATAGTACCGCGCGTGCAGTGGACTGTGGGGGCTGGCGTGTGATGTAC	1510
OY	338	GluMetMetCysGIlyArgLeuProPheTyrAsnGlnAspHisGluValLeuPheGluLeu	357
Db	1511	GAGATGAGTGGGTGGCTGGCTGCTCTTCAACCAAGACCAATGAGAACCTTTTGAGCTC	1570
OY	358	IleLeuMetGIuAspIleIleValPheProAsnIlePheThrIleuSerSerAspAlaIysSerIleuLeu	377
Db	1571	ATCTTCATGAGAGAAATCCGCTTCCCGGCAAGCTTGCTGGTCCGAGGCGCAAGCTTGCTT	1630
OY	378	SerGIlyLeuLeuIleIleValAspProAsnIleValArgLeuGIlyGIlyProAspAspAlaIys	397
Db	1631	TCAGGGCTGCTCAAGAAAGACCCCAAGACGAGCGTTGGCGGGGCTCCGAGAGCGCCAG	1690
OY	398	GluIleMetCysArgHisSerPhePheSerGIlyValAsnTyrGlnAspValTyrAspIlyIys	417
Db	1691	GAGATCATGACGACATCGCTTCTTGGCCGGTATCGGTGGCAGCACTGTACAGACGAAGAG	1750
OY	418	LeuValProProPheValProGlnValThrSerGIuThrAspThrArgTyrPheAspGlu	437
Db	1751	CTCAGCCCACTTCAAGCCCAAGGTCAAGTCGACGAGACTGACACCGAGTATTTGAGTAG	1810
OY	438	GluPheThrAlaGlnThrIleThrIleThrProProGluIlyTyrAspGIuAspGIyMet	457
Db	1811	GAGTTCACGGCCACAGATGATCACCATCAACCACTGACCAA-----GATGACGAGATG	1864
OY	458	AspCysMetAspAsnGluValArgProHisPheProGlnPheSerTyrSerAlaSerGIly	477
Db	1865	GAGTGTGTGACAGCAGGACGACGAGGCCCACTTCCGCCAGTTCTCTACTCGGCGACGCGC	1924
RESULT 7			
US-10-324-985A-1			
Sequence 1, Application US/10324985A			
Publication No. US20030144204A1			
GENERAL INFORMATION:			
APPLICANT: Spencer, David			
TITLE OF INVENTION: Act-based Inducible Survival Switch for Gene Therapy			
FILE REFERENCE: P03248US1/10106761			
CURRENT APPLICATION NUMBER: US/10/324,985A			
CURRENT FILING DATE: 2002-12-19			
PRIOR APPLICATION NUMBER: US 60/342,155			
PRIOR FILING DATE: 2001-12-19			

	NUMBER OF SEQ ID NOS: 12	
/	SOFTWARE: PatentIn version 3.1	
/	SEQ ID NO 1	
/	LENGTH: 2626	
/	TYPE: DNA	
/	ORGANISM: mouse	
US-10-324-985A-1		
 Alignment Scores:		
Pred. No.:	6.86e-228	Length: 2626
Score:	2100.50	Matches: 396
Percent Similarity:	90.00%	Conservative: 36
Best Local Similarity:	82.50%	Mismatches: 43
Query Match:	82.11%	Gaps: 5
Dbl:	15	Indels: 4
 US-09-869-079B-3 (1-479) x US-10-324-985A-1 (1-2626)		
QY	1 MetSerAspValThrIleValLeuGluGlyTrpValGlnValArgGlyGluTyrIleLeu	20
DB	284 ATGAACGACGTAGCCATTGTAAAGAGGGCTGGCGCAAAACGAGGGAAATATTTTAA	343
QY	21 AsnTPAqPProArqTYrPheLeuLeuYthrAspGlySerPheIleGTYrtyrGlu	40
DB	344 ACCTGCCGCCACGCCTACTTCCTCTCAAGAAGATGGCACCCTTATTGGCTACAAGAA	403
QY	41 LysPProGlnAspValAsp---LeuProTYrProLeuAsnAsnPheSerValAlaLysCyS	59
DB	404 CGGCTCATGAGTAGTGAGATCACGAGAGTCCCACATAAACATCTTCTACGTGGCAATGC	463
QY	60 GlnLeuMetLysThrgLuArgProLysProAsnThrPheIleIleArgCYsLeuGlnTrp	79
DB	464 CAGCTGATGAAGACAGAGCGGCCAAAGCCCAAACCTTATATCATCCGCTGCATGG	523
QY	80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThr	99
DB	524 ACCACAGTCATTGAGCGCACCTTCATGTGAAGACCTGAGAGCGGGAAAGATGGGCC	583
QY	100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCys	119
DB	584 ACCGCCATTACAGTCTGGCCGATGAGCTCAAGAGCGAGAAAGAACATGATGACTTC	643
QY	120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis	139
DB	644 CGATCAGGCTCACCAAGTACACTCAGGGGCTGAAGATGAGTGTCTCCGTGGCAAG	703
QY	140 HisLys---ArgLysThrMetAsnAspPheAspTYrLeuLysLeuLeuGlyLysGlyThr	158
DB	704 CCCAAGACCCGTGACCATTAAGAGTTTGAATACCTGAACCTAATCTGGCAAGGCCAC	763
QY	159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTYrTYrAlaMetCysIle	178
DB	764 TTGGGAAAGTCATTCTGTGTAAAGAAAGGCCACAGGCCCTACTATGCCATGAAGTCC	823
QY	179 LeuLysLysGluValIleIleAlaLysAspGluValAlaniStrhLeuThrGlnSerArg	198
DB	824 CTCAAGAAAGAGTCATGTCGCCAAGATGAGTGGCCACACAGCTTACAGAAACGCT	883
QY	199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTYrSerPheGlnThrLys	218
DB	884 GTCTCTCGAAGACTAGGCATCCCTTCTTACGGCCCTCAAGTACTCTTCACAGCCAC	943
QY	219 AspArgLeuCysPheValMetGluTYrValAsnGlyGlyGluLysPheHisLeuSer	238
DB	944 GACCGCTCTGTCTTGTCATGAAGTATGCCAACGGGGCGAGCTCTTCCACCTGCTCT	1003
QY	239 ArgGluArgValPheSerGluAspArgThzArgPheTYrGlyAlaGluIleValSerAla	258
DB	1004 CGAAGCGCGGTCTTCTCCGAGAACCGGGCCCGCTTATATGTGGAGAAATTGTGTCTCC	1063
QY	259 LeuAspTYrLeuHisSerGlyLys---IleValTYrArgAspLeuLysLeuGluAsnLeu	277
DB	1064 CTGACATCACTTGACCTCCGAGAAAGACGTGTGTACCGGAGCTCGAAGCTGAGAACTCC	1123

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QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
    |||||
DB 1124 ATCTGAGCAAGAGACCGGCAATCAAGATACGAGCTTGGGCTGTGCAGAGAGGGGATC 1183
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGluuTyLeuAlaProGluVal 317
    |||||
DB 1184 AAGGATGTGTGCTCACTATGAAGACATTCGTGGGAAACCGGAGTACCTGGCCCTGAGGTG 1243
QY 318 LeuGluAspAsnAspArgTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyr 337
    |||||
DB 1244 CTGGAGAGCAACGACACTACGCGCTGTGCAAGAGCTGTGGGGCTGGGCTGTGCAATGAT 1303
QY 338 GluMetMetCysGlyYArgLeuProPheTyrAsnGluAspHisGlyuLysLeuPheGluLeu 357
    |||||
DB 1304 GAGATATGTGTGGCCGCTGCTGCTTCTACACAGAGACCAAGAGAGCTGTTCGAGCTG 1363
QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
    |||||
DB 1364 ATCTCATGTGAGGAGATCCGCTTCCGCGACACTCGGCCCTGAGGCCAAGTCCCTGCTC 1423
QY 378 SerGlyLeuLeuLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLys 397
    |||||
DB 1424 TCCGGGCTGCTCAAGAGAGACCTTACACAGAGCTGTGGGGCTGTGAGATGCAAG 1483
QY 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGluAspValTyrAspLysLys 417
    |||||
DB 1484 GAGATATGTGTGAGACCGGCTTCTTGTCCACATGTGTGTGGCAGATGTGTATGAGAGAG 1543
QY 418 LeuValProProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
    |||||
DB 1544 CTGAGGCCACCTTCAAGCCCGGCTGCTGACCTGAGACTGACACAGTATTTCATGAG 1603
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
    |||||
DB 1604 GAGTTCACAGCTCAGATGATCACCATCACGCGCTGATCAA-----GATGACAGCATG 1657
QY 458 AspCysMetAspAsnGluArgArgProHisPheProGluPheSerTyrSerAlaSerGly 477
    |||||
DB 1658 GAGTGTGTGACAGCATGACGGGAGGCGGCACTTCCCAAGTTCCTCTACAGCAGATGGC 1717

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RESULT 8
US-10-713-678-5
; Sequence 5, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10/713,678
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-713-678-5

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Alignment Scores:

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Pred. No.: 6,866-228 Length: 2626
Score: 2100.50 Matches: 396
Percent Similarity: 90.00% Conservative: 36
Best Local Similarity: 82.50% Mismatches: 43
Query Match: 82.11% Indels: 5
DB: 18 Gaps: 4

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US-09-869-079B-3 (1-479) x US-10-713-678-5 (1-2626)

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QY 1 MetSerAspValThrIleValLysGluGlyTyrValGlnLysArgGlyGlyuTyTrpIleLys 20
    |||||
DB 284 ATGAAGAGAGTATGCCATTTGTGAAGAGAGGCTGGCTGCAAAACGAGGGGAATTTATTA 343
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
    |||||
DB 344 ACCGTGGCGGCAACGCTACTTCTCTCTCAAGAACGATGCGACCTTTATTTGGCTACAGGA 403
QY 41 LysProGluAspValAsp---LeuProTyrProLeuAsnAspPheSerValAlaLysCys 59
    |||||
DB 404 CGAGCTCAGATGTGATGATAGCGAGAGATCCCACTCAACACTTCTCAATGTGGACATATC 463
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleArgCysLeuGlnTrp 79
    |||||
DB 464 CAGCTGATGAAGACAGAGGCGCAAGGCCCAACACTTTATCATCGCTGCTGAGGTG 523
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGlyGlyuTyTrpThr 99
    |||||
DB 524 ACCACAGTCATGAGCGCACCTTCCATGTGTGAACGCTGAGAGCGGGAGAGATGGGCC 583
QY 100 GluAlaIleGluAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCys 119
    |||||
DB 584 ACCGCCATTCAAGCTGTGGCCGATGAGACTCAAGAGCGAGAAAGAGACGATGACATTC 643
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 139
    |||||
DB 644 CGATCAGGCTCACCCAGTACCAACTCAGGGGCTGAAGATGAGAGTGTCCCTGGCCAG 703
QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLysGlyLysGlyThr 158
    |||||
DB 704 CCCAAGCACACGCTGTGACCATGAAACGATGTGATCTGMAACTGAGGCAAGGCGCAC 763
QY 159 PheGlyLysValIleLeuValArgLysLysValAsnGlyLysTyrTyrLysMetLysIle 178
    |||||
DB 764 TTGGGAAGATATTTGTGTGAAGAGAGGACAGGCGGCTGACTATGCTATGCAAGAGATC 823
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
    |||||
DB 824 CTCAGAGAGAGATGATGTGCTCCCAAGATGAGATGAGTTGCCACAGCTTCTAGAAACGT 883
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
    |||||
DB 884 GTCTGTCAGAACCTCAGGATCCCTTCTTACGCGCTTCAAGTACTCATTCAGACCCAC 943
QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyGlyLeuPhePheHisLeuSer 238
    |||||
DB 944 GACCGCTGTGCTTGTGATGAGATGCAAGAGGAGGAGGAGCTTCTTCCACCTGTCT 1003
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
    |||||
DB 1004 CGAGAGCGGCTGTGCTCCGAGAGACCGGCGCTTCTATGAGTGGAGATTTGATCTGCTGCC 1063
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
    |||||
DB 1064 CTGGACTACTTCCACTCCAGAGAAACGAGTGTACCGGAGACTGAGACTGAGAACTTC 1123
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
    |||||
DB 1124 ATCTGAGCAAGAGACCGGCAATCAAGATACGAGCTTGGGCTGTGCAGAGAGGGGATC 1183
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGluuTyLeuAlaProGluVal 317
    |||||
DB 1184 AAGGATGTGTGCTCACTATGAAGACATTCGTGGGAAACCGGAGTACCTGGCCCTGAGGTG 1243
QY 318 LeuGluAspAsnAspArgTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyr 337
    |||||
DB 1244 CTGGAGAGCAACGACACTACGCGCTGTGCAAGAGCTGTGGGGCTGTGCAATGAT 1303
QY 338 GluMetMetCysGlyYArgLeuProPheTyrAsnGluAspHisGlyuLysLeuPheGluLeu 357
    |||||
DB 1304 GAGATATGTGTGGCCGCTGCTGCTTCTACACAGAGACCAAGAGAGCTGTTCGAGCTG 1363
QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377

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Db 1604 GAGTTCACAGCTCAGATGATGATCAACATCACGCCCTGATCAA-----GATGACAGCATG 1657

QY 458 AASPcYMeTAspAnGluArgProHISpHeProGlnPheSerTyrSerAlaSerGly 477

Db 1658 GAGTGTGTGACAGTGAAGGAGGCGCACTTCCCAAGTTCTTCACTCAGCAAGTGGC 1717

RESULT 10

US-10-895-225A-56

Sequence 56, Application US/10895225A

Publication No. US20050048587A1

GENERAL INFORMATION:

APPLICANT: Rao, Patricia

APPLICANT: Snyder, Jessica

APPLICANT: Bagley, Andria

TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE

TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR

FILE REFERENCE: TLN-025

CURRENT APPLICATION NUMBER: US/10/895,225A

CURRENT FILING DATE: 2004-07-19

PRIOR APPLICATION NUMBER: 60/488,502

PRIOR FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PaateSeq for Windows Version 4.0

SEQ ID NO 56

LENGTH: 2626

TYPE: DNA

ORGANISM: Homo sapiens

US-10-895-225A-56

Alignment Scores:

Pred. No.: 6,866-228 Length: 2626

Score: 2100.50 Matches: 396

Percent Similarity: 90.00% Conservative: 36

Best Local Similarity: 82.50% Mismatches: 43

Query Match: 82.11% Indels: 5

DB: 19 Gaps: 4

US-09-869-079B-3 (1-479) x US-10-895-225A-56 (1-2626)

QY 1 MetSerAspValThrIleValysGluGlyTyrValGlnLysArgGlyGlyTyrIleLys 20

Db 284 ATGAACAGACGTACCACTGTGAAGAGGCTGCTGCACAAACGAGAGGAAATATTATAA 343

QY 21 AsnTyrArgProArgTyrPheLeuLeuLysTyrAspGlySerPheIleGlyTyrLysGlu 40

Db 344 ACCTGGCGGCGACGCTACTTCTCTCCAGAGAGATGGACCTTTATGGCTTCAAGAA 403

QY 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnAsnSerValAlaLysCys 59

Db 404 CGGCTCAGAGATGTGATCAGCAGAGAGTCCCACTCAACAACTTCACTGCGCAATGC 463

QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79

Db 464 CAGCTATGAAGACAGAGCGGCGCAAGGCCCAACACCTTTATCATCCGCTGCTGCAATGC 523

QY 80 ThrThrValIleGlnArgThrPheHisValAspThrProGlnGluArgGlnGluTyrPThr 99

Db 524 ACCACAGTCAATTAGGGGACCTTCCATGTGAAACCGCTGAGAGGGGAAAGATGGGCC 583

QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlnGluGluArgMetAsnCys 119

Db 584 ACCGCATTCAGACTGTGGCGGATGACTCAACAGAGGAGGAGAAAGACGATGCACTTC 643

QY 120 SerProThrSerGlnIleAspAsnIleGlyGlnGlnGlnMetSerAspAlaSerThrHis 139

Db 644 CGATCAGGCTCACCCAGTGAACACTAGAGGGCTGAAGAGATGAGGTCTCCGCGCAAG 703

QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyTyr 158

Db 704 CCAGACGACCGGTGTGACCAAGAGAGTGTGAGTACTGAAATACCTAGGGCAAGGGCAC 763

QY 159 PheGlyLysValIleLeuValArgGluLysArgLysSerGlyLysTyrAlaMetLysIle 178

Db 764 TTTGGAAAGTATTCTGTGAAAGAGAGGCCACAGGCCCTACTATGCATGAAGATC 823

QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArg 198

Db 824 CTCAGAGAGAGTCACTGTCGCAAGATGAGTGGTCCCAACGCTTACTGAGAACCT 883

QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218

Db 884 GTCTCGACAACTCAAGGATCCCTTCCCTTACGGCCCTCAAGTACTCATTTCCAGACCAC 943

QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyGlnLeuPhePheHisLeuSer 238

Db 944 GACCGCTCTGCTTTGTCTATGAGATGCAACGGGGGGAGACTCTTCTTCCACCTGTCT 1003

QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258

Db 1004 CAGAGCGCGTGTCTTCCAGAGACCGGCCCTTCTATGTGCGGAGATTTGTGTGCC 1063

QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGlnLeu 277

Db 1064 CTGACTACTTGCATCCGAGAAAGACGTGTGTACCGGGACTGAAAGCTGGAGAACCTC 1123

QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlyIle 297

Db 1124 ATGCTGACAGAGACGGGACATCAAGATMACGACTTGGCTGTGCAAGAGGGGATC 1183

QY 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGlyTyrLeuAlaProGluVal 317

Db 1184 AAGATGTGTGCCATTTGAGAGACATTTCTGCGAACCGCGAGTACTTGGCCCTGAGGTG 1243

QY 318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrTyrGlyLeuGlyValValMetTyr 337

Db 1244 CTGAGAGACAAACGACTACGCGCTGACAGTGTGAGTGTGGGGCTGGGCTGTGCATGAT 1303

QY 338 GlnMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlnLysLeuPheGluLeu 357

Db 1304 GAGATGATGTGTGGCGCTGCTTCTTCAACACGAGACCAAGAGAGCTTTCAGAGCTG 1363

QY 358 IleLeuMetGluAspIleLysAspPheProArgTyrThrLeuSerSerAspAlaLysSerLeu 377

Db 1364 ATCTCATGAGAGAGATCCGCTTCCGCGCAACCTGCGCCCTGAGGCCAAGTCCCTGCTC 1423

QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397

Db 1424 TCCGGGCTGCTCAAGAGAGACCTTACAGAGAGCTGCGTGGGGGCTGAGGATGCCAAG 1483

QY 398 GlnIleMetArgHisSerPheSerGlyValAsnTyrGlnAspValTyrAspLysLys 417

Db 1484 GAGATCATCAGACACCGGTTCTTGTCCCAACATCGTGTGACAGATGTATGAGAGAG 1543

QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437

Db 1544 CTGAGGCCACTTTTCAAGGCCCAAGCTTCACTTGAAGTGAACCAAGATTTCCATGAG 1603

QY 438 GlnPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457

Db 1604 GAGTTCACAGCTCAGATGATCAACATCAGCGCGCTGATCAA-----GATGACAGCATG 1657

QY 458 AASPcYMeTAspAnGluArgProHISpHeProGlnPheSerTyrSerAlaSerGly 477

Db 1658 GAGTGTGTGACAGTGAAGGAGGCGCACTTCCCAAGTTCTTCACTCAGCAAGTGGC 1717

RESULT 11

US-10-072-036-70

Sequence 70, Application US/10072036

Publication No. US20030082564A1

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP

APPLICANT: Sara BURON

APPLICANT: Soren TULLIN

APPLICANT: Kasper ALMHOLT

APPLICANT: Kurt SCUDDER

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I


```

1 TITLE OF INVENTION: On A Cellular Responses
2
3 FILE REFERENCE: 3759-0120P
4
5 CURRENT APPLICATION NUMBER: US/10/072,036
6
7 PRIOR FILING DATE: 2002-09-13
8
9 PRIOR APPLICATION NUMBER: 09/417,197
10
11 PRIOR FILING DATE: 1999-10-07
12
13 NUMBER OF SEQ ID NOS: 143
14
15 SOFTWARE: PatentIn version 3.0
16
17 SEQ ID NO: 70
18
19 LENGTH: 2181
20
21 TYPE: DNA
22
23 ORGANISM: Artificial Sequence
24
25 FEATURE:
26
27 OTHER INFORMATION: PKB-EGFP fusion
28
29 FEATURE:
30
31 NAME/KEY: CDS
32
33 LOCATION: (1)..(2178)
34
35 US-10-072-036-70

```

Alignment Scores:			
Pred. No.:	6,78e-228	Length:	2181
Score:	2099.50	Matches:	396
Percent Similarity:	90.19%	Conservative:	36
Best Local Similarity:	82.67%	Mismatches:	42
Query Match:	82.08%	Indels:	5
DB:	14	Gaps:	4
US-09-869-079B-3 (1-479) x US-10-072-036-70 (1-2181)			
QY	1	MeLSeRAspValThrIleValLySGInGIYTPValGInLYeARGIYGIuTYrIleLys	20
Db	1	ATAGAGCACTGCTATTGTGAAGGAGGTTGCTGCACAAACGAGGAGTACATCAAG	60
QY	21	AsnTPARgProKrgYrPheLeuLeuLYSThARpGIYSePheIleGIYTYrLYeGIu	40
Db	61	ACCTGGCGGCAAGCTACTTCTCTCCACAAATGATGGACCTTCATTGGCTACAGAG	120
QY	41	LYeProGIInAspValAsp--LeuProTYrProLeuAsnAsnPheSeValAlaLysCys	59
Db	121	CGGCGGCAAGATGTGACCAAGTGAAGTCCCTCCACACACTTCTCTGTGGCCAGTGC	180
QY	60	GInLeuWeLYSThGIuArGPProLYSPRoAsnThrPheIleIeArGIYSeuGIuTYr	79
Db	181	CAGCTATGAAGCGAGCGCGCCGCCCAACCTTCATCATCCGCTGCTCAGTGG	240
QY	80	ThTThValIleGIuArGThrPheHsValAspThrProGIuArGIuArGIuTYrThr	99
Db	241	ACCACGTATCAAGACGACCTTCCATGTGGAGTCTCTGGAGAGCGGAGAGATGACA	300
QY	100	GIuAlaIleGIuAlaValAlaAspArgLeuGIuArGInGIuArGIuArGLeuMetAsnCys	119
Db	301	ACCGCATCCAGCTGTGGCTGACGGCTCCAAAGAGCAGAGAGAGAGATGACTTC	360
QY	120	SePProThSeRGIInLeAspAnIleGIYGIuGIuGIuMetAspValSeThrThIs	139
Db	361	CGGTGGGCTCACCCAGTGAACCTCAGGGGCTGAAGAGATGAGAGTGTCCCTGGCCAG	420
QY	140	HisLYe--ArgLYSThMetAsnAspPheAspTYrLeuLYeLeuGIYLYeGIYThr	158
Db	421	CCCAACACCGCGCTGACCATGAACGAGTTTGAGTCTCGAAGCTGTGGGCAAGGGCACT	480
QY	159	PheGIYLYeValIleLeuValArgGIuLYsAlaSeRGIYLYrTYrAlaMetLYeIle	178
Db	481	TTGGGCAAGTATCTGTGTGAAGAGAGAGCCACAGGCCGTACTACGCATTAAGTC	540
QY	179	LeuLYeLYeGIuValIleIleAlaLYsAspGIuValAlaHsThLeuThGIuSeArX	198
Db	541	CTCAAGAAAGGAGTATCTGTGGCCAAAGCAGAGTGGCCACACACTCAGAGAACCGC	600
QY	199	ValLeuLYeAsnThrArgHsProPheLeuThrSeRLeuLYrTYrSePheGIuThLYs	218
Db	601	GTCTCTCAAGATCCAGGACCCCTTCTCCACAGGCCGAGAGTATCTTTCCAAACCCAC	660

QY 219 AaprhagLeuCySPheValMetGluTyrValAsnGlyGlyGluLeuPhePheHisIleAsnSer 238
 Db 661 GACCGCTCTGCTTTGTCATGAGATACCGCAACGGGGGGGAGACTGTTCTTCCACTGTGTC 720
 QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyValAGluIleValSerAla 258
 Db 721 CGGAGACGTGTGTTCTCCGAGGACCGGGCCCGCTTCTATGGCGCTGAGATTGTGTACGCC 780
 QY 259 LeuAspTyrLeuHisSerGlyIleValIleValIleValIleValIleValIleValIleVal 277
 Db 781 CTGGACTCTACCTGCACTCCGAGAGAAACGTGGGTACCGGGGACCTCAACCTGGAGAAACCTC 840
 QY 278 MetLeuAspTyrAspArgGlyHisIleIleValIleThrAspPheGlyLeuCysIleGlyIle 297
 Db 841 ATGCTGGCAAGAACGGGCACTTAAGATCAACAAGCTTCGGGCTGTGCAAGAGAGGGGATTC 900
 QY 298 ThrAspAlaIleThrMetLeuThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
 Db 901 AAGACCGGTGCCACCATGAAGACCTTTGGCGGCAACCTGAGTACTGTGGCCCCGAGGTG 960
 QY 318 LeuGluAspAsnAspTyrGlyValArgAlaValAspTyrTPDgIleuGlyValValMetTyr 337
 Db 961 CTGGAGGACATATGACTACGAGCGGTGCACTGAGCATGTGGGGGCTGGGCGTGTATGATGAC 1020
 QY 338 GluMetMetCysGlyArgLeuProPheTyrTrpAsnGluAspHisGluIleLeuPheGluLeu 357
 Db 1021 GAGATGATGATGTCGGTCCGCTGCTCCCTTCTACCAACGAGACCAAGAAAGCTTTTGGCTTC 1080
 QY 358 IleLeuMetGluAspIleValPheProArgThrIleSerSerAspAlaIleSerLeuLeu 377
 Db 1081 ATCTCTATGAGAGAGATCCGCTTCCCGGCAAGCTTTGGTCCGAGGCCAAGTCTTGCTT 1140
 QY 378 SerGlyLeuLeuIleValAspProAsnLysArgLeuGlyGlyIleProAspAlaIle 397
 Db 1141 TCAGGGCTGCTCAAGAAAGACCCCAAGCAGAGGCTTTGGCGGGGCTCCGAGACCGCAAG 1200
 QY 398 GluIleMetArgHisSerPhePheSerGlyValAsnTyrGluAspValTyrAspLysLys 417
 Db 1201 GAGATCAAGACGATCGCTTCTTTCGCGGTATCGTGTGGCAGCAAGTGTACAGAAAGAAAG 1260
 QY 418 LeuValProProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
 Db 1261 CTCAGCCCACTTCAGACCCCAAGGTCAAGTGGAGACTGACACCAAGGATTTGATGAG 1320
 QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
 Db 1321 GAGTTTCAAGCGCCAGATGATCATCATCACTACCACTGACCA-----GATACAGCAGATG 1374
 QY 458 AspCysMetAspAsnGluArgArgProHisPheProGluPheSerTyrSerAlaSer 476
 Db 1375 GAGGTGTGTGACAGCAGCAGCGCAGCGCCCACTTCCCGGATTCCTACTCGGCCAGC 1431

RESULT 12
 US-10-072-036-138
 ? Sequence 138, Application US/10072036
 ? Publication No. US20030082564A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Ole THASTRUP
 ? APPLICANT: Sara BJORN
 ? APPLICANT: Soren FULIN
 ? APPLICANT: Kasper ALMHOLT
 ? APPLICANT: Kunt SCUDDER
 ? TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
 ? FILE REFERENCE: 3759-0120P
 ? CURRENT APPLICATION NUMBER: US/10/072,036
 ? CURRENT FILING DATE: 2002-09-13
 ? PRIOR APPLICATION NUMBER: 09/417,197
 ? PRIOR FILING DATE: 1999-10-07
 ? NUMBER OF SEQ ID NOS: 143
 ? SOFTWARE: PatentIn version 3.0.
 ? SEQ ID NO 138
 ? LENGTH: 2184


```

/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: EGFP-PKX fusion
/ NAME/KEY: CDS
/ LOCATION: (1)..(2181)
US-10-072-036-138

Alignment Scores:
Pred. No.: 6,79e-228 Length: 2184
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 14 Gaps: 4

US-09-869-079B-3 (1-479) X US-10-072-036-138 (1-2184)

QY 1 MetSerAspValThrIleValIysGluGlyTyrValGlnIleAspGlyGluTyrIleIys 20
DB 742 ATGAGCGAGCTGCTGATTTGTAAGAGGGTGGCTGCACAAAGAGGGAGTACATCAAG 801
QY 21 AsnTPArgProArgTyrPheIleuLeuIysThrAspGlySerPheIleGlyTyrIleGlu 40
DB 802 ACCGTGGCGGCACGGCTACTTCTCCCAAGATGATGGCAGCTTCATTGGCTACAGAGAG 861
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaIysCys 59
DB 862 CGGCGCGAGATGTGAGCAACAGCTGAGGCTCCCTCAACACTTCTCTGTGGCGCAGTGC 921
QY 60 GlnLeuMetIleThrGlnArgProIysProAsnThrPheIleIleArgCysLeuGlnTyr 79
DB 922 CAGCTGATGAAGCGAGGCGGCCCGCCCAACACTTCATCATCCGCTGCGTGCAGTGG 981
QY 80 ThrThrValIleGlnArgThrPheIleValAspThrProGlnGlnArgGluTyrThr 99
DB 982 ACCACGTGATGAGAGCAGCACTTCCATGTGAGACCTCTGAGAGGAGGAGGAGTGGACA 1041
QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnIleGlnIleArgLeuMetLeuIys 119
DB 1042 ACCGCGATCCAGACTGTGGTGAAGGCGCTCAAGACAGAGAGAGAGAGATGACATTC 1101
QY 120 SerProThrSerGlnIleAspAsnIleGlyGlnGlnIleMetAspAlaSerThrThr 139
DB 1102 CGTGGCGGCTCACCCAGTGAACACTCAGGGGCTGAGAGATGAGGTGCTCCGCGCAG 1161
QY 140 HisIys---ArgIleThrMetAsnAspPheAspTyrLeuIleuLeuGlyIysGlyThr 158
DB 1162 CCCAGACACCGGTGACATGAACGAGTTGAGTACCTGAGCTGTGGGCAAGGCGACT 1221
QY 159 PheGlyIleValIleLeuValArgGluIysAlaSerGlyIysTyrTyrAlaMetIysIle 178
DB 1222 TTCGGAGAGTATCTGTGTGAAGAGAGGAGCCAGCGCGCTACTACCGCATGAAGATC 1281
QY 179 LeuIleValGluValIleIleAlaIysAspGluValAlaHisThrLeuThrGlnSerArg 198
DB 1282 CTCAGAGAGAGAGTATCTGTGTGAAGAGAGGAGCCAGCGCGCTACTACCGCATGAAGATC 1341
QY 199 ValLeuIleAsnThrArgHisProPheLeuThrSerLeuIysTyrSerPheGlnThrIys 218
DB 1342 GTCCTGCAACACCCAGGACCCCTTCTCCACAGCCCTGAGTACCTTCCAGAGCCAC 1401
QY 219 AspArgLeuCysPhePheIleMetGluTyrValAsnGlyIleGlnLeuPhePheHisLeuSer 238
DB 1402 GACCGCGCTCTGCTTGTGATGAGTACGCCAACGGGGGCGAGGTGTCTTCCACCTGTCC 1461
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 1462 CGGGAACGTGTGTTCTCCGAGGACCGGGGCCGCTTCTTATGAGGCGCTGAGATTGTGAGCC 1521
QY 259 LeuAspTyrLeuHisSerGlyIys---IleValTyrArgAspLeuIysLeuGluAsnLeu 277

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DB 1522 CTGACATACCTGCACTCGGAGAGAAAGCTGTGTATCCGGGACCTCAAGCTGAGAACTTC 1581
QY 278 MetLeuAspIleAspGlyHisIleIleIysIleThrAspPheGlyLeuCysIleGluIle 297
DB 1582 ATGCTGAGCAAGAGAGCGGAGCACTTAAGATCAAGACTTCGGGCTGTGCAAGAGAGGAGATC 1641
QY 298 ThrAspAlaIleThrMetIleThrPheCysGlyIleThrProGlnTyrLeuAlaProGluVal 317
DB 1642 AAGGACGGGTGCACATGAGACCTTTGGCGGACACCTGAGTACCTGGCCCCCGAGGTG 1701
QY 318 LeuGluAspAsnAspTyrGlyArgAlaValaAspTyrPheGlyIleValIleMetTyr 337
DB 1702 CTGAGAGAAATGACTACGCGCGTGAAGTACGTGAGTGGGGCTGGCGTGGATGATGAC 1761
QY 338 GlnMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyIleIysLeuPheGluLeu 357
DB 1762 GAGATGATGTGGGTGCGCTGCGCTCTTCAACACAGACAGACATGAGAGCTTTTGAAGTCC 1821
QY 358 IleLeuMetGluAspIleIlePheProArgThrLeuSerSerAspAlaIleIysSerLeuLeu 377
DB 1822 ATCTCATAGAGAGATCCGCTTCCCGGCGCAGCTTGTGTCGAGGCGCAAGTCTTGTGCTT 1881
QY 378 SerGlyLeuLeuIleIleAspProAsnIysArgLeuGlyIleGlyIleProAspAspAlaIys 397
DB 1882 TCAAGGCTGTCAAGAAAGACCCCAAGCAGAGGCTTGGGGGGGCTCCAGAGACCGCAG 1941
QY 398 GlnIleMetArgHisSerPhePheSerGlyValaAsnTyrGlnAspValTyrAspIysIys 417
DB 1942 GAGATCATGACACATCGCTTCTTCCGCTACGTGTGCGACACAGTGTACAGAGAAAG 2001
QY 418 LeuValProProPheIleAspProGlnIleValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 2002 CTCACGCCACCTTCAAGCCCAAGGTGACGTGAGACTGACACAGGATATTTGATGAG 2061
QY 438 GlnPheThrAlaGlnThrIleThrIleThrProProGlnIleIleIleAspGluIleMet 457
DB 2062 GAGTTCACGGCCCAAGATGATCAATCAACACCACTGAGCA---GATGACAGCATG 2115
QY 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 2116 GAGTGTGTGAGACAGAGAGGCGAGGCCCACTTCCCGCAGTTCTCTACTGCGCAGC 2172

RESULT 13
US-09-970-000-3
; Sequence 3, Application US/09970000
; Patent No. US20020127214A1
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian Arthur
TITLE OF INVENTION: Rac-Protein Kinase as Therapeutic Agent
Or In Diagnostics
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: No. US20020127214A1aIatis Patent and Trademark Department
STREET: 564 Morris Avenue
CITY: Summit
STATE: NJ
COUNTRY: USA
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/970,000
FILING DATE: 03-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/068,702
FILING DATE: 13-May-1998
APPLICATION NUMBER: PCT/EP96/04810
FILING DATE: 11-May-1996
APPLICATION NUMBER: GB 9523379.7
FILING DATE: 16-May-1995

```

APPLICATION NUMBER: GB 9525704.4
 FILING DATE: 15-Dec-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Furman, Diane E.
 REGISTRATION NUMBER: 31,104
 REFERENCE/DOCKET NUMBER: 4-20635/A/PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 522-6924
 TELEFAX: (908) 522-6955
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2610 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Human RAC alpha
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 199..1641
 NAME/KEY: mat_peptide
 LOCATION: 199..1641
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-970-000-3

Alignment Scores:
 Pred. No.: 8,846-228 Length: 2610
 Score: 2099.50 Matches: 396
 Percent Similarity: 90.19% Conservative: 36
 Best Local Similarity: 82.67% Mismatches: 42
 Query Match: 82.08% Indels: 5
 DB: 9 Gaps: 4

US-09-869-079b-3 (1-479) x US-09-970-000-3 (1-2610)

QY 1 MetSerAspValThrIleValysGluGlyTTPValGlnLysArgGluGlyTyrIleLys 20
 DB 199 ATGAGGAGCTGCTTGTGTGAGAGGTTGCTGCACAAAGAGGAGTACATCAG 258
 QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
 DB 259 ACCTGGCGGCAAGCTTACTTCCCTCCCAAGATGATGGACCTTATTTGGCTACAGAG 318
 QY 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
 DB 319 CGGCCCCAGAGATGTGACCAACCTGAGGCTCCCTCAACAACTTCTGTGGCGCAGTGC 378
 QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTTP 79
 DB 379 GAGCTATGAGAGCGAGGCGGCCGCCCAACACCTTCACTCCGCTGCGCAGTGC 438
 QY 80 ThrThrValIleGlnArgThrPheIleValAspThrProGlnGlnArgGlnGluTyrPThr 99
 DB 439 ACCACGTGTCATGAAAGCACTTCCATGTGAGACCTCTGAGAGGCGGAGAGTGTGACA 498
 QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlnGluGlnArgMetAsnCys 119
 DB 499 ACCGCATCCAGACTGTGGCTGACCGGCTCCAAAGACAGAGAGAGAGATGAGACTTCC 558
 QY 120 SerProThrSerGlnIleAspAsnIleGlyGlnGlnGlnMetAspAlaSerThrThrHis 139
 DB 559 CGGTGGGCTCACCCAGTGCACCTCAGAGGCGTGAAGAGATGAGGTGTCTCCGCGCAAG 618
 QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyTyr 158
 DB 619 CCCAAGCACCGCGTGAACATGAACGAGTTTGAAGTACGTGAAGTGTGCGGCAAGGCGACT 678

QY 159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIle 178
 DB 679 TTCCGCAAGCTGATCTCTGTTGAGAGAGGCAAGGCCCTACTTACCGCATGAAGATC 738
 QY 179 LeuLysLysGlnValIleIleAlaLysAspGlnValAlaIleThrLeuThrGlnSerArg 198
 DB 739 CTCAGAGAGAGATGATCTGTGGCAAGAGACGAGGTGGCCCACTACCTCCAGAACCCG 798
 QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
 DB 799 GTCTCTGCAACTCCAGGACCCCTTCTCCACAGCCTTAAGATCTTCTCCAGACCAC 858
 QY 219 AspArgLysCysPheValMetGluTyrValAlaGlnGlyLysLeuPhePheHisLeuSer 238
 DB 859 GACCGCTCTGCTTGTCTATGAGATGCGCAACGGGGGGAGCTGTCTTCCACCTGTCC 918
 QY 239 ArgGlnArgValPheSerGlnAspArgThrArgPheTyrGlyValAlaGlnIleValSerAla 258
 DB 919 CCGGAACGTGTGTCTCCAGAGACCGGGCCCGCTTCTATGGCGTGAATTTGTGTACGCC 978
 QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGlnAsnLeu 277
 DB 979 CTGACTTACTCTGACTCGAGAAAGACGTGTGTACCGGACCTCAAGCTGGAGAACCTTC 1038
 QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuLysGlnGlyIle 297
 DB 1039 ATGCTGGAACAAGACCGGCACTTAAGATCACAGACTTGGGTGTGCAAGAGGGAGATC 1098
 QY 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGlnTyrLeuAlaProGlnVal 317
 DB 1099 AAGAGCGTGCCACCATGAAGACCTTTTGGGCAACCTGAGTACTGGCCCCCGAGGATC 1158
 QY 318 LeuGlnAspAsnAspTyrGlyValArgAlaValAspTTPTrpGlyLeuGlyValValMetTyr 337
 DB 1159 CTGAGAGCAATGACTACCGCGCTGACGTGACGTGGGGCGTGGCTGTGCATGATAC 1218
 QY 338 GlnMetMetCysGlyValArgLeuProPheTyrAsnGlnAsnHisGlnLysLeuPheGlnLeu 357
 DB 1219 GAGATGATGTGGGTGCTGCTGCTTCTTCAACACAGAGACCATGAAGCTTTTGAAGCTC 1278
 QY 358 IleLeuMetGlnAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
 DB 1279 ATCTCATGAGAGAGATCCGCTTCCCGGCAAGCTTGTGCTCCGAGGCCAAGTCTTGGCT 1338
 QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLys 397
 DB 1339 TCAGGGCTGCTCAAGAGAGACCCCAAGAGGCTTGGCGGGGCTCCGAGGACGCGCAAG 1398
 QY 398 GlnIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLys 417
 DB 1399 GAGATCATGACATCGCTTCTTGGCGGTATCGTGTGACAGACGTGACAGAGAGAG 1458
 QY 418 LeuValProProPheLysProGlnValThrSerGlnThrAspThrArgTyrPheAspGln 437
 DB 1459 CTCAGGCCACCTTCAAGCCCAAGGTACGTGAGACGTGACACCAAGATTTTATGAGAG 1518
 QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGlnLysTyrAspGlnAspGlyMet 457
 DB 1519 GAGTTCACGGCCCAAGATGATCATCATCACACCACTGACCAA-----GATGACACAGT 1572
 QY 458 AspCysMetAspAsnGlnArgArgProHisPheProGlnPheSerTyrTrpSerLysSer 476
 DB 1573 GAGTGTGTGAACAGAGGAGGCGGCCCACTTCCCAAGTTCCTTACCTGGCCAGC 1629

RESULT 14
 US-10-388-263-329
 ; Sequence 329, Application US/10388263
 ; Publication No. US20030228597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowser, Lex M.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: McNeill, John
 ; APPLICANT: Freier, Susan M.

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/ APPLICANT: Sasmor, Henri M.
/ APPLICANT: Brooks, Douglas G.
/ APPLICANT: Ohashi, Cara
/ APPLICANT: Wyatt, Jacqueline R.
/ APPLICANT: Borchers, Alexander
/ APPLICANT: Vickers, Timothy A.
/ TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
/ TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
/ FILE REFERENCE: ISIS-4503
/ CURRENT APPLICATION NUMBER: US/10/388,263
/ FILING DATE: 2003-03-12
/ NUMBER OF SEQ ID NOS: 947
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 329
/ LENGTH: 2610
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (199) ... (1641)
US-10-388-263-329

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Alignment Scores:
Pred. No.: 8,84e-228 Length: 2610
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 17 Gaps: 4

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US-09-869-079B-3 (1-479) x US-10-388-263-329 (1-2610)

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QY 1 MetSeAspValThrIleValysGluGlyTrpValGlnIleAspGlyGluTrpIleIys 20
DB 199 ATGAGGAGAGTGGCTATGTGGAGAGGTTGGCTCACAAAGAGGAGATCATCAAG 258
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrIysGlu 40
DB 259 ACCTGGCGGACGACTACTTCCCTCCCAAGATGATGAGCATCTTATGGCTACAAAGAG 318
QY 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
DB 319 CGGCCCCAGAGATGTGACCAACGTGAGGCTCCCTCAACAACCTTCTGTGGCGCAGTGC 378
QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79
DB 379 CAGCTATGAGAGCGAGGCGGCCCCGAGCCCAACACTTCATCATCCGCTGCGCAGTG 438
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpThr 99
DB 439 ACCACGTGATGAGAGCAACCTTCATGTGAGACCTCTGAGAGGCGGAGAGATGAGAC 498
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCys 119
DB 499 ACCGCATCCAGACTGTGGCTGAGCGGCTCAAGAAACAGAGAGAGAGATGAGACTTC 558
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrTrpHis 139
DB 559 CGGTCCGGCTCAACCGTGAACCTGAGGGGCTGAAAGATGAGGTGCTCTGGCCAAAG 618
QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluGlyLysGlyThr 158
DB 619 CCCAAGACCGCGGTGACATGAAAGAGTTGAGTACTGAGCTGTGGCAAGGCGACT 678
QY 159 PheGlyLysValIleLeuValArgGluValAspSerGlyLysTyrTyrAlaMetLysIle 178
DB 679 TTCGGCAAGGTGATCTGTGTGAAGAGAGGCGGCGCTAATACGCATGAGATGC 738
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisPheThrLeuThrGluSerArg 198
DB 739 CTCAGAGAGAGATCATCTGTGCGCAAGAGAGAGTGGCCACACTCCAGGAACCGC 798

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QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
DB 799 GTCTGGCAAGACTCCAGGACCCCTTCCCTCAAGCCCTGAAGTACTCTTCCAGACCAG 858
QY 219 AspArgLeuCysPheValMetGluTyrValaAsnGlyGlyLeuPhePheHisLeuSer 238
DB 859 GACCGCTCTGCTTGTCTATGAGTACCGCAACGGGGGGGAGCTGTTCTCACCTGTC 918
QY 239 ArgGluArgValPheSerGlnAspArgThrArgPheTyrGlyValaGluIleValSerAla 258
DB 919 CCGAAGCTGTGTTCTCCAGGACCGGGCCCTTCTATGGCTGAGATTGTCTACGCC 978
QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 979 CTGGAATACCTGCACTCGGAGAAAGACGAGTGTACCGGGAGCTCAAGCTGAGAAACCTC 1038
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
DB 1039 ATGCTGAGCAAGAGAGCGGCACTTAAGATCACAGACTTCGGCTGTGCAAGAGGGGATC 1098
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyTyrTrpGluTyrLeuAlaProGluVal 317
DB 1099 AAGGACGCTGCCACATGAGACCTTTTGGGCAACCTGAGTACTGAGCTCCCGAGGTG 1158
QY 318 LeuGluAspAsnAspTyrGlyArgAlaValaAspTrpTrpGlyLeuGlyValaMetTyr 337
DB 1159 CTGAGGACAAATGACTACGCGCTGTGAGTGAAGTGTGGGGCTGGGCGTGTGATGTAC 1218
QY 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeu 357
DB 1219 GAGATGATGTGGGTGCTGCTGCTTCTTCAACACAGGACCATGAGAAAGCTTTTGTGCTC 1278
QY 358 IleLeuMetGluAspIleLysPheProArgTrpTrpLeuSerSerAspAlaLysSerLeuLeu 377
DB 1279 ATCTTCATGAGAGAGTCCGCTTCCCGGACGCTTGTGCTCCGAGGCCAAGTCTTGTCT 1338
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAlaLys 397
DB 1339 TCAGGCGCTCTCAAGAGAGCCCAAGAGAGCTTGGGGGGGCTCCGAGAGCGCCAG 1398
QY 398 GluIleMetArgHisSerPheSerGlyValaAsnTrpGlnAspValTyrAspLysLys 417
DB 1399 GAGATCATGACACTGCTCTTGTGCGGTATCGTGTGACACAGCTGATCAAGAAAG 1458
QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 1459 CTCAGCCCACTTCAAGCCCAAGTCACTGAGACTGAGACAGACAGGATTTTGTATGAG 1518
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1519 GAGTTCAGGCGCCAGATGATGATCACTACACACCACTGACCA-----GATGACAGCATG 1572
QY 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 1573 GAGTGTGTGAGACAGAGAGCGGCGGCCCACTTCCCAAGTCTCTTACTGCGGCAGC 1629

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RESULT 15

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US-10-641-1206
/ Sequence 1206, Application US/10641643
/ Publication No. US20040077003A1
/ GENERAL INFORMATION:
/ APPLICANT: Cocks, Benjamin G.
/              Susan G. Stuart
/              Jeffrey J. Seilhammer
/ TITLE OF INVENTION: GENE EXPRESSION
/              COMPOSITION FOR THE DETECTION OF BLOOD CELL
/ NUMBER OF SEQUENCES: 1508
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA

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      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/641,643
      FILING DATE: 14-Aug-2003
      CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: <Unknown>
      FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
      NAME: Zeller, Karen J.
      REGISTRATION NUMBER: 37,071
      REFERENCE/DOCKET NUMBER: PA-0001 US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (650) 855-0555
      TELEFAX: (650) 845-4166
      INFORMATION FOR SEQ ID NO: 1206:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 2610 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      IMMEDIATE SOURCE:
      LIBRARY: GENBANK
      CLONE: g190827
      SEQUENCE DESCRIPTION: SEQ ID NO: 1206 :
US-10-641-643-1206

Alignment Scores:
      Pred. No.:      8.84e-228      Length:      2610
      Score:          2099.50         Matches:      396
      Percent Similarity: 90.19%      Conservative: 36
      Best Local Similarity: 82.67%    Mismatches:  42
      Query Match:      82.08%        Indels:       5
      DB:                17           Gaps:         4

US-09-869-079B-3 (1-479) x US-10-641-643-1206 (1-2610)
QY      1 MetSerAspValThrIleValLysGluGlyTrpValGlnLysAspGlyGluTrpIleLys 20
DB      199 ATAGAGCACTGCTATTTGAAAGAGGTTGGCTGCACAACGAGGGGAGTACATCAAG 258
QY      21 AsnTrpArgProArgTrpPheLeuLeuLysThrAspGlySerPheIleGlyTrpLysGlu 40
DB      259 ACCTGGGGGCGACGCTACTTCTCTCTCAAGAAATGATGGCACCTTCATTGGCTACAGAG 318
QY      41 LysProGlnAspValAsp--LeuProTrpProLeuAsnAsnPheSerValAlaLysCys 59
DB      319 CGGCGCGAGATGTGGACCAACGTGAGGCTCCCTCAACAACCTTCTGTGGCGGAGTGC 378
QY      60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleLeuGlySerLeuGlnTrp 79
DB      379 CACCTGATGAAGAGCGGCGGCGGCCCAACACCTTCATCACTCGCTCGCACTGG 438
QY      80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThr 99
DB      439 ACCACGTGATCGAAGCGCACTTCATGTGAGAGCTCTCAGAGAGCGGAGAGATGGACA 498
QY      100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetAsnCys 119
DB      499 ACCGCGCATCGACGTGGCTGACCGGCTCAAGAGAGAGAGAGAGAGAGATGAGACTTC 558
QY      120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrpHis 139
DB      559 CGGTGGGCTTCAACCACTGACATCAAGGAGCTGAAGAGATGAGAGTCTCGGCCCAAG 618
QY      140 HisLys--ArgLysThrMetAsnAspPheAspTrpLeuLysLeuGluGlySerGlyThr 158
DB      619 CCGAAGACCGGCGGAGACCATGAACGATTTGAGTACTGAAGCTGCTGGGCAAGGGCACT 678
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QY      159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTrpTrpAlaMetLysIle 178
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QY      179 LeuLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
DB      739 CTCAAGAGAGATCATCTGGGCCAAGAGAGAGAGTGGCCACACATCACCAGAACCCG 798
QY      199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTrpSerPheGlnTrpLys 218
DB      799 GTCCTGAGAACTCCAGGACCCCTTCTCTCAAGCCGTGAAGTACTCTTCCAGACCCAC 858
QY      219 AspArgLeuCysPheValMetGluTrpValAsnGlyGlyGluPhePheHisLeuSer 238
DB      859 GACCGGCTCTGCTTGTCTCATGAGTACGCCACAGGGGGCGAGGTGTTCTTCCACTGTCC 918
QY      239 ArgGluArgValPheSerGluAspArgTrpArgPheTrpGlyValAlaGluIleValSerAla 258
DB      919 CGGAAACGTGTGTTCTCCAGAGACCGGGCCGCTTATGGCCCTGAGATTTGTCTAGCC 978
QY      259 LeuAspTrpLeuHisSerGlyLys--IleValTrpArgAspLeuLysLeuGluAsnLeu 277
DB      979 CTGAGACTACTGCACTCGAGAGAGAAAGTGGTGTACCGGGACTCAAGCTGAGAACTCC 1038
QY      278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
DB      1039 ATGCTGACAAAGACCGGACCATTAAGATCAAGACTTCGGGCTGTGCAGAGGGGATC 1098
QY      298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluVal 317
DB      1099 AAGAGCGGTGCCCACTGAAGACCTTTTGGGACACCTGAGTACTTGGCCCCCGAGGTG 1158
QY      318 LeuGluAspAsnAspTrpGlyArgAlaValAspTrpTrpGlyLeuGlyValAlaMetTrp 337
DB      1159 CTGAGAGACATATGACTACGCGCGTGCAGTGAAGTGGGGGGCTGGGCGGTGATGATAC 1218
QY      338 GlnMetMetCysGlyArgLeuProPheTrpAsnGlnAspHisGluLysLeuPheGluLeu 357
DB      1219 GAGATGATGTGGCGGTGCTGCTCTTCAACACGAGACCATGAGAGCTTTTGTAGCTC 1278
QY      358 IleLeuMetGluAspIleLysPheProArgTrpLeuSerSerAspAlaLysSerLeuLeu 377
DB      1279 ATCTCATGAGAGAGATCCGCTTCCGCGACCGCTTGTCGCCAGGCCAAGTCTTGCTT 1338
QY      378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397
DB      1339 TCAAGGCTGTCTCAAGAGAGACCCCAAGAGAGAGCTTGGGGGGGCTCCAGAGACGCCAAG 1398
QY      398 GlnIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTrpAspLysLys 417
DB      1399 GAGATCATGAGCATGCTTCTTTCGCGGTATGTGTGGACGACGATGACGAGAAAG 1458
QY      418 LeuValProProPheLysProGluValThrSerGlnThrAspThrArgTrpPheAspGlu 437
DB      1459 CTCAGCCCACTTCAAGCCCAAGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1518
QY      438 GlnPheThrAlaGlnThrIleThrIleThrProProGluLysTrpAspGluAspGlyMet 457
DB      1519 GAGTTCACGCGCCCAAGATGATCAACATCAACACCACTGACCA-----GATGACAGCATG 1572
QY      458 AspCysMetCAspAsnGluArgArgProHisPheProGlnPheSerTrpSerAlaSer 476
DB      1573 GAGTGTGTGACAGCAGAGCGAGCGCCCACTTCCCAAGTTCCTTACTCGGCCAAG 1629
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Job time : 719 secs

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JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1445)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louie, H., Kowals, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAX Plate: 13 Row: b Column: 23
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923313
 This clone has the following problem: no polyA-tail.

FEATURES
 source 1..1445
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3867931"
 /cissue_type="Eye, retinoblastoma"
 /clone_lib="NIH MGC_67"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"

ORIGIN

Alignment Scores:

Pred. No.: 5,24e-279 Length: 1445
 Score: 2462.00 Matches: 461
 Percent Similarity: 99.57% Conservative: 3
 Best Local Similarity: 98.93% Mismatches: 2
 Query Match: 96.25% Indels: 0
 DB: 3 Gaps: 0

US-09-869-079b-3 (1-479) x BC020479 (1-1445)

QY 1 MetSerAspValThrIleValysGluGlyTTPValGlnIlyAsrGlyGlyTyrIlelys 20
 DB 47 ATGAGCGATGTTACCACTTGGAAGAAGGTTGGGTCAGAGAGGGAGAAATATATAA 106
 QY 21 AantTArGPrArGrYrPheLeuLeuYrThAspGlySerPheIleGlyTyrIlysglu 40
 DB 107 AACTGAGGCCAAGATTAATCTCTTTGGAAGACAGATGGCTCATTCATAGATATAAAG 166
 QY 41 LysPProGlnAspValAspLeuProTyrProLeuAsnAsnPheserValAlalyCyssGln 60
 DB 167 AAACCTCAAGATGTGAATTAATCTATCCCTCAACACATTTTCATGGCAAAATGCCAG 226
 QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyrThr 80
 DB 227 TTAACCAAAACAAGACAGACCAAGCAACACATTTATATACAGATGTCTCCAGTGACT 286
 QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGlnTyrPThrGlu 100
 DB 287 ACTGTTATAGAGAACTTATCTATGTAGTAATCTCCAGAGAAAGGAGAAATGAGACAGA 346

QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
 DB 347 GGTATCCAGGCTGTAGACAGACTGCAGAGCAAGAGAGAGAGATGATGTACT 406
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
 DB 407 CCACTTCAACAATGATATATAGAGAGAGAGAGATGAGCCCTTCAACACCCATCAT 466
 QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
 DB 467 AAAGAGACACATGATATATTTTGACTATTTGAACCTACAGTAAAGGACCTTTGGG 526
 QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
 DB 527 AAAGTTATTTTGTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 586
 QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
 DB 587 AAAGAGTCATTTATGCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 646
 QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 DB 647 AAAGACACTAGACATCTCTTTTAACTCTGAAATATCTCTTCCAGACAAAGACCT 706
 QY 221 LeuCyPheValMetGluTyrValAsnGlyGlyLeuPhePheHisLeuSerArgGlu 240
 DB 707 TGTGTTTGTATGGAATATGTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766
 QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
 DB 767 CCGGTTCTCTGAGAGACCGACAGCTTCTATGTCGAGAAATGTCCTCTCCCTTGAC 826
 QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
 DB 827 TATCTACATTCGCGAAGAGATGTGTACCTGATCTCAAGTTCAGAGATTAATGCTGGAC 886
 QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCyLysGluGlyIleThrAspAla 300
 DB 887 AAAGATGGCACATATAAATTAACAGATTTTGACCTTGGCAAGAGAGATCAAGATGCA 946
 QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
 DB 947 GCCACCATGAAAGACATCTGTGGCACTCCAGAAATATCTGGACACAGAGGTGTAAGAT 1006
 QY 321 AsnAspTyrGlyArgAlaValAspTyrTPGlyLeuGluValValMetTyrGluMetMet 340
 DB 1007 AATGACTATGGCCGAGCACTAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1066
 QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
 DB 1067 TGTGGAGGTTACCTTTCTACACACAGACAGACAGAACTTTTGATTAATTAATTAATG 1126
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
 DB 1127 GAAGCATTAATTTCTCGAACACTCTCTTCAAGTGCAGAAATCATGTCTTCAAGGCTC 1186
 QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLysGluIleMet 400
 DB 1187 TTGATTAAGGATCCAAATTAACGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1246
 QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLysLeuValPro 420
 DB 1247 AGACACAGTTCTTCTCTGAGTAACCTGCAAGATGATATGATATAAAGCTTGTAACCT 1306
 QY 421 ProPheLysPProGlnValHisSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
 DB 1307 CCTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTGATGATAAATTTTAA 1366
 QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
 DB 1367 GCTCAGACTATTAACATTAACACCACTGAAAATATGATGAGATGATGAGATGCAATG 1426
 QY 461 AspAsnGluArgArgPro 466

Db 1427 GACAAATGAGGCGGCCG 1444

RESULT 2
AY399351 1440 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY399351 GI:39755340
VERSION AY399351.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1440)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene titros
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS 2 (bases 1 to 1440)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Score: 2368.00 Matches: 450
Percent Similarity: 93.95% Conservative: 0
Best Local Similarity: 93.95% Mismatches: 29
Query Match: 92.57% Indels: 0
Gaps: 0
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Db 61 AACTGAGGCCAAGATACCTCTTTTGAAGACAGATGGCTCATTCATAGATATTAAGAG 120
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QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
Db 601 AAGACACTAGACATCCCTTTTAAACATCTTGAAATATTCCTTCCAGACAAAGACCGT 660
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DEFINITION	Mus musculus AKT3 gene, VIRUTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY399353		
VERSION	AY399353.1		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1394)		
	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.		
TITLE	Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.		
	Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
REFERENCE	14671302		
AUTHORS	2 (bases 1 to 1394)		
	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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	/locus_tag="HGM0195"		
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	Pred. No.: 2,976-256	Length: 1394	
	Score: 2269.00	Matches: 432	
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	DB: 9	Gaps: 0	
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QY	37	GIYTYrYlYsGluYsProGlnAspValAspLeuProYrProLeuAsnAenPheSerVal	56
Db	63	GGCTTAAAGGAGAAACCTCAAGATGGAGCTTAACCTTACCCCTCAACACTTCACAG	122
QY	57	AlAlYsCYsGlnLeuMetLysThrGluYrGProLYsProAsnThrPheTleTleYrCYs	76
Db	123	GCAAAATGTCACTTAATGAAAAAGACAGACCAAGGCCAAATATCATTTATTCAGATCT	182
QY	77	LeuGlnTTPThrThrValIleGluYrThrPheHsValAspThrProGluGluYrGlu	96
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OY	137	ThrThrHisHisAlaValArgLysThrMetAsnAspPheAspArgLysLeuLysLeuGluLys	156
Db	363	ACAACCCATCATTAAGAAAGACGATTAAGATTGTTACATTATTTGAAACATCAAGTAA	422
OY	157	GlyThrPheGlyLysValIleLeuValArgGluLysLaseGlyLysTyrValMet	176
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Db	483	AAGATTCTGAAGAAGATCATATTATTCGAAAGATAGATGAGCGACACACTCTTACGAA	542
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OY	277	LeuMetLeuAspArgLysArgLysIleLysIleThrAspPheGlyLeuCysLysGluGly	296
Db	783	TTGATGCTAGATTAAGATGCGCCATATATAAATTACGATTTTGGCTTTCGAAAGAGG	842
OY	297	IleThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGlu	316
Db	843	ATCACAGATGACGCTACCATGAAGACACTTGTGGCACACAGAGTACCTGGCACAGAG	902
OY	317	ValLeuGluAspAsnAspArgTyrGlyArgAlaValAlaAspTrpTrpGlyLeuGlyValValMet	336
Db	903	GTATTAGAAAGTAAATGACTATGGCCGAGCCGTGGACGTGGGGCTTAAGGTGTATG	962
OY	337	TyrGluMetMetCysGlyArgSerLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGlu	356
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Db 1383 GGACGGGAA 1391

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LOCUS
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proto-oncogene 1, full insert sequence.

ACCESSION
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VERSION
AK040758.1 GI:26333954
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636

REFERENCE
AUTHORS
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159

REFERENCE
AUTHORS
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishi, K., Kitesunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
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Yoneoka, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861

TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
JOURNAL
Nature 409, 685-690 (2001)
PUBMED
11076861

REFERENCE
AUTHORS
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
PUBMED
11076861

TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
JOURNAL
Analysis of the mouse transcriptome based on functional annotation
of 6,770 full-length cDNAs
PUBMED
11076861

REFERENCE
AUTHORS
5 Nature 420, 563-573 (2002)

TITLE
Analysis of the mouse transcriptome based on functional annotation
of 6,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
PUBMED
11076861

REFERENCE
AUTHORS
6 (bases 1 to 1848)
TITLE
Adachi, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hasegaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hironaka, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,
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Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohnishi, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

COMMENT
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
Kanagawa 220-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location: Qualifiers

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US-09-869-079b-3 (1-479) x AK040758 (1-1848)

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Qy      298 ThrAspAlaIleThrMetLysThrPheCyseGlyThrProGluTyrLeuAlaProGluVal 317
Db      1077 AAGGACGGTCCCATAGAGACATCTTGGGAAACCCGGAGATCTGGGCCCTTGAGGAG 1136
Qy      318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrPrgLysGlyValValMetTyr 337
Db      1137 CTGGAGAGACACGACCTACGGCGGTGAGTGTGTGGGGCTGGGGCTGGTCACTGTC 1196
Qy      338 GluMetMetCyseGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeu 357
Db      1197 GAGATGATGTGTGGCCGCTGCTCTTCAACACAGACACACAGAAAGCTGTTCCAGCTG 1256
Qy      358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db      1257 ATCTCATGAGAGAGATCCGCTTCCGCGACACTCGGCCCTGAGGCCAAGTCCCTGCTC 1316
Qy      378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLys 397
Db      1317 TCCGGGCTGCTCAAGAAAGACCTTACAGAGGCTCGTGTGGGGCTCCAGAGATTCCAAAG 1376
Qy      398 GluIleMetArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLys 417
Db      1377 GAGATCATCAGACACCGTCTTTCCTTGCACATCTGTGGCAGAGATCTGATGAGAAAG 1436
Qy      418 LeuValProProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
Db      1437 CTGAGCCCACTTTCAGGCCCGAGTCACTGAGACTGACACCGAGTATTTCCATGAG 1496
Qy      438 Glu-PheThrAlaGlnThrIleThrIleThrProGluLysTyrAspGluAspLys 457
Db      1497 GAGTTTCAAGCTCAATATATCATCAACGCGGCTGAT----- 1536
Qy      457 tAspCyseMetAspAsnGluArgArgProHisPheProGln-PheSerTyrSerAlaSerG 477

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Db      1537 -----CAAATTCTTACTACGACCGATG 1559
Qy      477 1y 477
Db      1560 GC 1561

RESULT 5
BC068106
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC068106
Danio rerio cDNA clone IMAGE:6996896.
1829 bp mRNA linear HTC 25-MAR-2004
BC068106.1 GI:45751578
HTC.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1829)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richard,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyshe,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A.C., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalka,U., Smalun,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1829)
Strausberg,R.
Direct Submission
Submitted (24-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Len Zou, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Odi Griffith, Ken Guin, Nancy Liao,
Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Worth,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabu,
Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,
Duane Smalun, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAK Plate: 147 Row: b Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein
This clone has the following problem: no cloning site /

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FEATURES	source	Location/Qualifiers
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Best Local Similarity:	76.034	Mismatches: 56
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DB:	3	Gaps: 5
US-09-869-079B-3 (1-479) x BC068106 (1-1829)		
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Db	153 ATGACGAGACCTCAAGTGTGTGAAGGAGGGCTGGCTCTTAAGAGAGGTGATCATCAAG	212
QY	21 AsntPParGProArgTyPheLeuleuLysthAspGlySerPheIleIleArgCysleuGlu	40
Db	213 ACATGAGGCCCCCGGATCTTCACTCCAGAGTACGAGCGCTCTTCACTGCGCTACAGAG	272
QY	41 LysPProGlnAspValAspleuPro--TyrProleuAsnaAspSerValAlaIysCys	59
Db	273 AAGCCGAGCTACCGACCGACGAGCTGTGACCCGCTCAACAACCTCTCTGTGAGAGAGTGT	332
QY	60 GlnleuMetLythThrgluArgProIysProAsnThrPheIleIleArgCysleuGlnTTP	79
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QY	80 ThrtThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTTPThr	99
Db	393 ACCACCGTCATTTAGCGGACCTTCCATGTGACAGACAGTACAGACGAGGACGAGTGATG	452
QY	100 GluAlaIleGlnAlaValAlaAspArgLeuGln--ArgGlnGluGluGluArgMetAsn	118
Db	453 CGAGCAATCCAAATGGTGGCCAAATGGGCTGCAGCGCGGGAGTGTGACGAGCCAAATGG	512
QY	119 CysSerProthSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThr	138
Db	513 ATCAAGTACAGCTCTCCACAGTGCCTGTGAGACATGAGATGTGTGTCTCAATCC	572
QY	139 HisHisAlaArgLyserThrMetAsnAspPheAspTyLeuIysleuIeuGlylysglyThr	158
Db	573 --ACGTCAGAGTGCAGATGATGACTTGTATCTTACCTGAAGCTGCTGGGAAAGGCGACG	629
QY	159 PheGlyLysValIleleuValArgGluYsAlaSerGlyLyserTyTyralaMetLysIle	178
Db	630 TTGGGAGAGGTATTTCTGGTGGCGGAGAGGCTCTGGGATGTACTACGCAAGAGATC	699
QY	179 LeuLySlyGluValIleIleAlaIysAspGluValAlaHisThrLeuThrGluSerArg	198
Db	690 CTGCCCAAGAGGTGATCTCGGAGAGATGAAAGTGGCGACACACTGCACAGAGAGTGA	749
QY	199 ValIleuLysAsnThrArgHisProPheLeuThrSerLeuIysTyPheSerPheGlnThrIys	218
Db	750 GGCTGCGAAGACCTAGACACCCCTTCTTACGACCTCAAAATACGCTTCCAGACTCAT	809
QY	219 AsPArgLeuCysPheValMetGluTyValAsnGlyGlyIleuAspPheHisLeuSer	238
Db	810 GACCGTCTGTCTTCTGCTATGAGATACGCCCAAGGTGAGAGACTATTTCTTCATCTGTCT	859
QY	239 ArgGluArgValPheSerGluAspArgThrArgPheTyGlyAlaGluIleValSerAla	258

Db	870	CGTGAAGCGTGTGTTCTCTGAGGAGTANAGAGCTCGCTTACCGCGCGTAGATGCTCTCTCT	922
Oy	259	LeuApTyTyrIleuHisSerGlyLysIleValTyrArgAspIleuLysLeuGluAsnLeuMet	278
Db	930	CTGACATCATCTGCACCTCAAGAAAGCGTGGTCTTACAGAGCCTGGAAGCTGGAACACCTCATG	989
Oy	279	LeuAspLysAspArgLysIleLysIleIleThrAspPheGlyLeuCybLysGluGlyIleLeuThr	298
Db	990	CTGATATATATGCGGACACATTTAAATACACAGACTTCGCTCTGTATTAAGAGGAAATCA	1049
Oy	299	AspAlaIleThrMetLysThrPheCysGlyThrProGluTyrIleuAlaProGluValLeu	318
Db	1050	GACGAGGCCACCATGAGAGACCTTCTGCGGAGACCCCAAGATTCCTTGGCCGGAGAGTCTGT	1108
Oy	319	GluAspAsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValValMetTyrGlu	338
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Oy	339	MetMetCysGlyValArgLeuProPheTyrAsnGlnAspHisGlyLysGlyLysPheGluLeuIle	358
Db	1170	ATGATGTGTGGCCCTCTGCGCTTCTTACAGTCACACACACGAGCGCTGTTCGACACAGATC	1229
Oy	359	LeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSer	378
Db	1230	GTTATGAGAGGAGATCCGCTTCCCGGACGCTTGAACACACCGCCAGAGCATCTGCTGACC	1289
Oy	379	GlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaLysGlu	398
Db	1290	GGCCTGCTGAGGAAGAAGCCCAACACAGAGCTGGCGGAGGCCCAAGATGATGCCAGAGAT	1349
Oy	399	IleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeu	418
Db	1350	GTCATGTATGCAACAGTTCTTCACGCGGGGCTTACAGGAGCATGTGTGTCAGAAAGACTG	1409
Oy	419	ValProProPheLysProGlnValIleThrSerGlnThrAspThrArgTyrPheAspGluGlu	438
Db	1410	CTGGCGCCCTTTAAACCGCAGGTACGTACAGAGCGGACACACCTCATTTGATGATGAG	1469
Oy	439	PheThrAlaGlnThrIleThrIleThrPheProGluLysTyrAspGluAspGlyMetAsp	458
Db	1470	TTCACCTGCGCAGACATCATCTGTGACCCCTCCAGACAG-----CTGAGC	1514
Oy	459	CysMetAspAsnGluArgArg-----ProHisPheProGlnPheSerTyrSerAla	475
Db	1515	TGTACAGACGCGAGAGAGTCTGGCGCATGCGACATTTCCCTCAGTTCTCTCATCGGCC	1574
Oy	476	SerGlyArgGlu 479	
Db	1575	AGCGTCCGAGAG 1586	
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DEFINITION	Pan troglodytes AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY399352		
VERSION	AY399352.1	GI:39755341	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		
TITLE	Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,		
	Adams,M.D. and Cargill,M.		
	Inferring nonneutral evolution from human-chimp-mouse orthologous		
	gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCES	2 (bases 1 to 1440)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		

Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Satsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Location/Qualifiers

1..1440

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

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/gene="AKT3"

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ORIGIN

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Percent Similarity:	69.31%	Conservative:	0
Best Local Similarity:	69.31%	Mismatches:	147
Query Match:	63.72%	Indels:	0
DB:	9	Gaps:	0

US-09-869-079b-3 (1-479) x AY39352 (1-1440)

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QY 21 AsnTPArgProArgTyrPheLeuLeuIysThrAspGlySerPheIleGlyTyrLeuGlu 40
DB 61 AACTGAGGCCAGATACCTTCCTTTGAGACAGATGCTCATTCAATGATATATAAGAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaIysCysGln 60
DB 121 AAACCTCAAGATGGATTACCTTATCCCTCAACACTTTCAATGGCAAAATCCCA 180
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
DB 181 TTAATATAAACAAGAACGACCAAGCAACATTAATATATATATATATATATATATATAT 240
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTTPThrGlu 100
DB 241 ACGTTATATAGAGACATTTTCATGTAGATCTCCAGAGAAAGGAAAGATGACAGAA 300
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetAspCysSer 120
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QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHisIle 140
DB 361 CCAACTCCCAAAATTAATATATATATATATATATATATATATATATATATATATAT 420
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QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuIys 180
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DB 601 AAGAACACATGACATCCCTTTTAAACATCTCTTAATAATTTCTCCAGACAAAAAGACCG 660
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QY 281 LysAspGlyHisIleIysIleThrAspPheGlyLeuCysLysGlyGlyIleThrAspAla 300
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QY 321 AsnAspTyrGlyArgAlaValAspTyrTyrGlyLeuGlyValIleMetTyrGluMetC 340
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QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
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QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMet 400
DB 1141 NNGATTAAGATCCAAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1200
QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLeuValPro 420
DB 1201 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260
QY 421 ProPheLysProGluValIleThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1261 CCTTTTAAACCTCAAGTAAATCATCTGACAGATACATGATATTTGATATAAGATTTTAA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB 1321 GCTCAGACTTATTCATATACATACACCTGAAATATATATATATATATATATATATAT 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
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RESULT 7
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DEFINITION AL545564 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
clone CS0D1015YL1 5-PRIME, mRNA sequence.
ACCESSION AL545564
VERSION AL545564.3 GI:45746045
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1136)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:11267399.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7252.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?w=CSODI015CF060P1&c=7252.r.

FEATURES

source

Location/Qualifiers

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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Alignment Scores:

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Pred. No.:      1,59e-169      Length:      1136
Score:          1533.00      Matches:      301
Percent Similarity: 87.37%      Conservative: 24
Best Local Similarity: 80.91%      Mismatches: 43
Query Match:      59.93%      Indels:      5
DB:              1          Gaps:      2

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US-09-869-079B-3 (1-479) x AL545564 (1-1136)

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QY 88 HisValAspThrProGluGluArgGluGluTrpThrGluAlaIleGlnAlaValAlaAsp 107
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DB 63 CATGTGAGACTCTCTAGAGAGCGGAGAGAGTGAACAACCCATTCAGACTGTGGCTGAC 122

QY 108 ArgLeuGlnArgGlnGluGluGluArgMetAsnCysSerProThrSerGlnIleAspAsn 127
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QY 128 IleGlyGluGluGluMetAspAlaSerThrHisHisIleLys--ArgLysThrMetAsn 146
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DB 183 TCAGGGGCTGAAGATGAGGTGCTCCCTGCGCAAGCCCAAGACCCGCGACCATGAAC 242

QY 147 AspPheAspTyrLeuLysLeuLysLeuGlyLysGlyThrPheGlyLysValIleLeuValArg 166
   :::::
DB 243 GAATTTGAGTACTGTAAGCTGCTGGGCAAGGCACTTTCGAGAGGTGATCTGCTGTAAG 302

QY 167 GluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLysGluValIleIleAla 186
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QY 187 LysAspGluValAlaHisThrLeuThrGluSerArgValLeuLysAsnThrArgHisPro 206
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DB 363 AAGAGAGAGGTGGCCACACACATCCAGAAACCGCTCTGAGAACTCCAGGACCC 422

QY 207 PheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArgLeuCysPheValMetGlu 226
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QY 227 TyrValAsnGlyLysLeuLysPheHisLeuSerArgLysValArgValPheSerGluAsp 246
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QY 247 ArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAspTyrLeuHisSerGlyLys 266
   :::::
DB 543 CGGAGCCGCTTCATGCGCTGAGATTGTGTCAAGCCCTGACATCACTGACCTCGAGAAAG 602

QY 267 ---IleValTyrArgAspLeuLysLeuGluLysLeuMetLeuAspLysAspGlyHisIle 285
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DB 663 AAGATCAAGACTTCGGGGCTGTGCAGAGAGGGGATCAAGGACGTCGCCACATGAAGACC 722
QY 306 PheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAspAsnAspTyrGlyArg 325
DB 723 TTTTGGGACACACTTAAGTACTGTCGCCCGGAGTCTGAGGACAAATGACTTCGGCCGT 782
QY 326 AlaValAspTyrTrpGlyLeuGlyValAlaMetTyrGluMetCysGlyArgLeuPro 345
DB 783 GCAGTGAAGCTGCGGGGGCTGGCGGTGATCAATGAGATGATGTCGGGTGCTGCCGCC 842
QY 346 PheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMetGluAspIleLysPhe 365
DB 843 TTTTCAACACAGACCAATGAGAAAGCTTTTGAAGCTCATCTTCATGAGAGAGATCCGCTTC 902
QY 366 ProArgThrLeuSer-SerAspAlaLysSerLeuLeuSerGlyLeuLeu-IleLysAsp 385
DB 903 CCGGCAAGCTGCTGCTCCCGAGGCAAGTCTTCTTTCAGGCTGCTCAGAGAGAGACC 962
QY 385 roAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMetArgHisSerPhe 405
DB 963 CCAAGCAGAGAGCTTGGCGGGGCTCCGAGAGAGCCCAAGAGATCATGACATCGCTTCT 1022
QY 405 heserGlyValAsnTrpGlnAspValTyrAspLysLysLeuValProProPheLysProG 425
DB 1023 TTCGCCGTATCGTGTGGSAGCMCGTGTACCAAAAAGCCACACCTTCACGCCCM 1082
QY 425 InValThrSerGluThrAspThrArgTyrPhe 435
DB 1083 G-GTTCGTGGGAGATTGACACCATGATATTT 1113

RESULT 8
AK028871
LOCUS
DEFINITION
MUS musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:473245F20 product:thymoma viral proto-oncogene 2,
full insert sequence.
ACCESSION
AK028871
VERSION
AK028871.1 GI:26324815
KEYWORDS
HTC; CAP trapper.
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Moshino, T., Harada, A.,
Yamamoto, R., Matsuno, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexed sequencing
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
MEDLINE
20530913
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Moshino, T., Harada, A.,
Yamamoto, R., Matsuno, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexed sequencing
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
MEDLINE
20530913

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PUBMED 11076861
 REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 688-690 (2001)
 REFERENCE 5
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3724)
 AUTHORS Aochi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hamaoka, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to. Prepare mouse tissues.
 URL: http://genome.gsc.riken.jp/ for further details.
 URL: http://genome.gsc.riken.jp/ Location/Qualifiers
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 Pred. No.: 1,85e-168 Length: 3724
 Score: 1530.50 Matches: 285
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 Best Local Similarity: 80.28% Mismatches: 33

Query Match: 59.83% Indels: 3
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 QY 145 MetAenAsPPhaSPtYrleuYsleuLengLylyGlyThPhaGlylyeValleleu 164
 DB 63 ATGAATGACTTCGATTATCTCAACCTCCGCGCAAGGACCTTCGGCAAGCTATTG 122
 QY 165 ValAsgLyAlaAseRgLylySTYrYrAlaMeLyIleleuYslysgLyValIle 184
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 QY 185 IleAlaYsaPgluValAlaIshleuThRhgluSerArgValleuYsaRthArg 204
 DB 183 ATTGCAAAAGATGAAGTCCGCCACACAGTCAAGAGACCGGGTCTCGCAATACCA 242
 QY 205 HisProPheLeuThSerleuYsYrSerPheGlnThLyAsPaRgLeuCySPheVal 224
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 QY 225 MetGluTyValAsnGlyglUleuPhePheIshleuSerArgGlyValPheSer 244
 DB 303 ATCGAGTACCCACCGGGGTGAGCTTTTCCACCTCTCCGAGGAGCTTTCACG 362
 QY 245 GluAsPaRgThArgPheTyRglValIleValSerAlaIleuAsPtyrleuHisSer 264
 DB 363 GAGGATCGGGCGGCTTTATGAGAGAGAGATTTGTCAGCTCGGATTTGCACTCG 422
 QY 265 GlyLyIleValTyArgPheleuYsleuGluAsPheMetleuAsPtyrleuYHs 284
 DB 423 AAGATGTGTGATCCGTACATCAAGCTGGAACCTTATGTGACAAAGTGGCCAC 482
 QY 285 IleLyIleThAsPhePheIleuCyLySGlyGlyIleThAsPalaIaIaThMeLyS 304
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 QY 325 ArgAlaValAsPtyrTgLyglUleuGlyValIleMetTyRglUmeMetCyegLyAsgLeu 344
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 QY 365 PheProArgThRleuSerSerAsPalaYsSerleuLeuSerGlyleuLeuIleYsaP 384
 DB 723 TTCGCGGACACTCGGCGCAGAGGCAAGTCCCTGCTGAGTCACTGGAAGAGGAC 782
 QY 385 ProAsnLyArgLeuGlyglYglYProAsPaRPaIaYleuGluIleuMetRghIshSerPhe 404
 DB 783 CCAAGACAGAGCTCGCGAGGTCCCAAGTATGCAAGAGAGTCTGAGCATATGATTC 842
 QY 405 PheSerGlyValAsnTgPglAsPValTyRAsPlySleuValProProPheLyPro 424
 DB 843 TTCCTCAGATCACTGCGAGAGACGTGTACAGAAAACCTCTGCAACCTTCAAACT 902
 QY 425 GlnValThSerGluThAsPthArgTyRpheAsPglUglUphetheThIaGlnThIle 444
 DB 903 CAGGTCACTTCAAGAGTGAACAAGGTACTTGTATGACGAGTTCACGCCCGAGTCCATC 962
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QY 465 ArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
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RESULT 9
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 LOCUS AGENCOURT 10157385 NIH_MGC_134 Mus musculus cDNA clone
 DEFINITION IMAGE:6518260 5', mRNA sequence.
 ACCESSION BUS20318
 VERSION BUS20318.1 GI:22827844
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 967)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-r@mail.nih.gov
 Tissue Procurement: Dr. David Rowe
 cDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM14039 row: 1 column: 05
 High quality sequence start: 16
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 this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 5,61e-168 Length: 967
 Score: 1519.00 Matches: 307
 Percent Similarity: 97.16% Conservative: 1
 Best Local Similarity: 96.85% Mismatches: 6
 Query Match: 59.38% Indels: 6
 DB: 5 Gaps: 0

US-09-869-079b-3 (1-479) x BUS20318 (1-967)

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 DB 26 TTGACATATTGAACTACTAGAGAA-GGCACCTTTGGGAAAGT-ATTGTTGTCGAGAG 83

QY 168 LysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLysGlyValIleIleAlaLys 187
 DB 84 AAGGCAAGTGGAAATACATATGCTATGAAAGATTCTGAAAGAAAGATCATTTGCAAG 143

QY 188 AspGluValAlaHisThrLeuThrGluSerArgValLeuLysAsnThrArgHisProPhe 207
 DB 144 GATGAAGTGGCAACACTCTTACTGAAAGCAGACTATAAGAACCAACATTCATTT 203

QY 208 LeuThrSerLeuLysTyrSerPheGlnThrLysAspArgLeuLysPheValMetGlyTyr 227
 DB 204 TTAACATCTTGAATATTCCTTCAGACAAAGACGTTTGTGTTTGTGATGATAT 263

QY 228 ValAsnGlyValGluLeuPhePheHisLeuSerArgGluArgValPheSerGluAspArg 247
 DB 264 GTTAAATGGCGAGAGCTGTTTTCATTTGTCCAGAGAGCGAGTCTCTCGAGACCG 323

QY 248 ThrArgPheTyrGlyValaGluIleValSerAlaLeuAspTyrLeuHisSerGlyLysIle 267
 DB 324 ACAAGTTTCTATGATGTCAGAAATATGCTCTGCTTGAGACTATCTCATCTGGAAGATT 383

QY 268 ValTyrArgAspLeuLysLeuGluIleAsnLeuMetLeuAspLysAspGlyHisIleLysIle 287
 DB 384 GTGTACCGTATCTCAAGTTGGAGAAATTTGATGCTGATAGAGATGCCATATAAAATT 443

QY 288 ThrAspPheGlyLeuLysLysGluGlyIleThrAspAlaAlaHisMetLysThrPheCys 307
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QY 308 GlyThrProGluLysLeuValaProGluValaLeuGluAspAspAspTyrGlyArgAlaVal 327
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QY 328 AspTyrTyrGlyLeuGlyValValaMetTyrGluMetMetCysGlyArgLeuProPheTyr 347
 DB 564 GACTGTGGGGCTTAGGTGTTGTCATGATGAATGATGTGGAGGTTGCCCTTTCTAC 623

QY 348 AsnGluAspHisGluLysLeuPheGluLeuIleLeuMetGluAspLysPheProArg 367
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QY 368 ThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeuLeuIleLysAspProAsnLys 387
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QY 388 ArgLeuGlyGlyGlyProAspAspAlaLysGluIleMetArgHisSer-PhePheSerGly 407
 DB 742 CGCCTTGTTGGAGGGCCAGATGATGCAAAAGATCATGAGCATATGTTTTTTCTCG 801

QY 407 ValaAsnTyrGlnAspValTyrAspLysLysLeuValProProPheLysProGlnValTh 427
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QY 427 rSerGluThrAspThr-ArgTyrPheAspGluGlu-PheThrAlaGlnThrIleThrIle 446
 DB 862 ATCTGAACAGACACCCCATATTTTGATGAAGAAATTTACGCTCAGACTATTACATA 921

QY 447 ThrProProGluLysTyrAspGluAspGlyMetAspCysMetAsp 461
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 LOCUS AL548951 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1042YE16 5-PRIME, mRNA sequence.
 ACCESSION AL548951
 VERSION AL548951.3 GI:45749360
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1015)
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:11270773.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequenage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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 was normalized. Library was constructed by Life Technologies, a

[illegible]

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Alignment Scores:
Pred. No.: 9,31e-159 Length: 1186
Score: 1442.00 Matches: 271
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Best Local Similarity: 78.55% Mismatches: 30
Query Match: 56.37% Indels: 6
DB: 3 Gaps: 4

US-09-869-079B-3 (1-479) x BC032709 (1-1186)

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DB 154 ATGAATGAGGTGTGTGTCATCAAGAGGCTGCTCCAGAGGCTGTAATCATCAAG 213
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DB 214 ACCTGAGAGCCAGGTCCTCTGCTGAGAGGAGGCTCTTCATTGAGTCAAGAG 273
QY 41 LysProGln-----AspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLys 58
DB 274 AGCCCGAGGCGCCCTGATCAGACTTACC---CCCTTAACAACCTTCTCGTAGCAGAA 330
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DB 451 ATCGGGCCCATCAGATGTGTGCGCAACAGCTCAGAGAGCGGCGCCAGGCGAGAGCC 510
QY 117 MetAsnCysSerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSer 136
DB 511 ATGACTTACAAAGTGTGCTCCCGCAAGTACTCTCCACGATGAGATGAGAGTGGCG 570
QY 137 ThrThrIleIleValArgLys---ThrMetAsnAspPheAspTyrLeuLysLeuGlu 155
DB 571 GTGACGAGGACGCGCTTAAGTGAATGATGATGATGATGATGATGATGATGATGATG 630
QY 156 LysGlyThrPheGlyIleValIleLeuValArgGluLysAlaSerGlyIleValIleVal 175
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QY 296 GlyIleThrAspAlaIleThrMetLysThrPheCysGlyTTPProGluTyrLeuAlaPro 315
DB 1051 GGCATCATGAGCGGCGCCACCATGAAACCTTCTGTGGAACCCCGAGATCACTGGCGCT 1110
QY 316 GluValIleGluLysAsnAspTyrGlyArgAlaValAspTyrTTPGlyLeuGlyVal 335
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RESULT 14

LOCUS BC040028 1297 bp mRNA linear HTC 18-NOV-2002
DEFINITION Homo sapiens, clone IMAGE:6020864, mRNA.
ACCESSION BC040028
VERSION BC040028.1 GI:25058955
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1297)

REFERENCE

AUTHORS Strausberg R.
TITLE Direct Substitution
JOURNAL Submitted (15-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadn@systemsbiology.org
Anup Madan, Jessica Fahy, Erin Halton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK Plate: 84 Row: n Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6715585
This clone has the following problem: no polyA-tail.

FEATURES

Location/Qualifiers
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/clone_lib="NIH_MGC_70"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 1,06e-158 Length: 1297
Score: 1442.00 Matches: 271
Percent Similarity: 89.57% Conservative: 38
Best Local Similarity: 78.55% Mismatches: 30
Query Match: 56.37% Indels: 6
DB: 3 Gaps: 4

US-09-869-079B-3 (1-479) x BC040028 (1-1297)

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QY 21 AsnTrpArgProArgTrpPheleuleuYThsAspGlySerPheIleGlyTrlyysGlu 40
DB 325 ACCTGAGGCCACGAGTACTTCCGTGTAAGAGGAGGAGGCTCTTCAATTGGGTACAGAGG 384
QY 41 LysProGln-----AspValAspLeuProTrpProleuAsnAsnPheserValAlalyS 58
DB 385 AGGCCCGAGGCCCTCATGACACTTACCC---CCCTTAAACAATCTTCCCGTAGAGAGAA 441
QY 59 CysGlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysleuGln 78
DB 442 TGCACACTATGAAAGCCAGAGGCCGCGCACCCCAACCTTGTCTATACGCTGCTGCGAG 501
QY 79 TrpThrThrValIleGluArgTrpPheHisValAspThrProGluGluArgGluGluTrp 98
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QY 99 ThrGluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlu-----GluGluArg 116
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QY 137 ThrThrHisIleLysArgLys--ThrMetAsnAspPheAspTrpLeuLysleuGly 155
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QY 156 LysGlyThrPheGlyLysValIleLeuValArgGluLysleuAspGlyLysTrpYraIa 175
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QY 176 MetLysIleLeuLysArgGluValIleIleAlaLysAspGluValAlaHisThrLeuThr 195
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QY 196 GluSerArgValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTrpSerPhe 215
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QY 336 MetTrpGluMetMet 340

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RESULT 15

CB520675

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

CB520675 820 bp mRNA linear EST 09-JUL-2003
 UI-M-G10-cej-b-10-0-UI.r1 NIH_BMAP_G10 Mus musculus cDNA clone
 IMAGE:6840203 5', mRNA sequence.

CB520675
 CB520675.1 GI:29354030
 EST

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NIH-MGC <http://mgs.nci.nih.gov/>

1 (bases 1 to 820)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Iln, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mouseefl.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5

Location/Qualifiers

1..820

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6840203"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP G10"

/note="Organ: Brain; Vector: PYX-Asc, Site_1: EcoR I;

Site_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into PYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is AGCGAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,

program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:
123e-156	820	269
Score:	1422.00	Conservative: 1
Percent Similarity:	98.90%	Mismatches: 3
Best Local Similarity:	98.53%	Indels: 0
Query Match:	55.59%	Gaps: 0

DB: 6

US-09-869-079B-3 (1-479) x CB520675 (1-820)

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QY 85 ArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGluAlaIleGlnAla 104

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Qy      165  ValArgGlnLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLysGlnValIle 184
Db      301  GTTCGAGAGAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 360
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Qy      225  MetGluTyrValIleGlnGlyGlyGlnPhePheHisLeuSerArgGlnValPheSer 244
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